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(57) Abstract

The present invention relates to a method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress resistance in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells. The present invention further relates to an isolated polynucleic acid obtainable by such a method as listed in Table 1 as well as recombinant polynucleic acid comprising the same. The present invention further relates to an isolated polypeptide encoded by a polynucleic acid of the invention. The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into a plant cell a recombinant DNA comprising a polynucleic acid as defined which when expressed in a plant cell enhances the tolerances or induces resistance to environmental stress conditions of said plant. The present invention particularly relates to plant cells, plants or harvestable parts or propagation material thereof transformed with a recombinant polynucleic acid as defined above.

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Genes involved in tolerance to environmental stress

The present invention relates to molecular biology, in particular plant molecular biology. In particular, the invention relates to improvements of crop productivity of useful plants. One of the major limitations of crop productivity is the effect of environmental stress conditions on plant growth and development. An important goal of molecular biology is the identification and isolation of genes that can provide resistance or tolerance to such stresses. For agriculture, the creation of transgenic plants containing such genes provides the potential for improving the stress resistance or tolerance of plants.

Drought, salt loading, and freezing are stresses that cause adverse effects on the growth of plants and the productivity of crops. The physiological response to these stresses arises out of changes in cellular gene expression. Expression of a number of genes has been demonstrated to be induced by these stresses (Zhu et al., 1997; Shinozaki et al., 1996; Thomashow, 1994). The products of these genes can be classified into two groups: those that directly protect against environmental stresses and those that regulate gene expression and signal transduction in the stress response. The first group includes proteins that likely function by protecting cells from dehydration, such as the enzymes required for biosynthesis of various osmoprotectants, late-embryogenesis-abundant (LEA) proteins, antifreeze proteins, chaperones, and detoxification enzymes (Shinozaki et al., 1997, Ingram et al., 1996, Bray et al., 1997). The second group of gene products includes transcription factors, protein kinases, and enzymes involved in phosphoinositide metabolism (Shinozaki et al., 1997). An overview of the methods known to improve stress tolerance in plants is also given in Holmberg & Bülow, (1998).

Further studies are definitely needed to give an insight into the mechanisms involved in the plant response to environmental stress conditions.

The study of plants naturally adapted to extreme desiccation has led to the hypothesis that the genetic information for tolerance to environmental stress conditions exists in all higher plants. In glycophytes, this information would only be expressed in seeds and pollen grains which undergo a desiccation process.

The induction of osmotolerance in plants is very important to crop productivity: 30 to 50 % of the land under irrigation is presently affected by salinity. Several lines of evidence also demonstrate that even mild environmental stress conditions throughout the growth season have a negative impact on plant growth and crop productivity. It is

for instance known that even minor limitations in water availability cause a reduced photosynthetic rate. Unpredictable rainfall, increase in soil salinity at the beginning and the end of the growing season often result in decreased plant growth and crop productivity. These environmental factors share at least one element of stress and that is water deficit or dehydration. Drought is a significant problem in agriculture today. Over the last 40 years, for example, drought accounted for 74% of the total US crop losses of corn. To sustain productivity under adverse environmental conditions, it is important to provide crops with a genetic basis for coping with water deficit, for example by breeding water retention and tolerance mechanisms into crops so that they can grow and yield under these adverse conditions.

It is an aim of the present invention to provide a new method for screening for plant genes involved in tolerance or resistance to environmental stress.

It is an aim of the present invention to provide new plant genes, more particularly plant genes providing the potential of improving the tolerance to environmental stress conditions in plants.

It is also an aim of the present invention to provide polypeptides encoded by said new plant genes.

It is further an aim of the present invention to provide methods for producing plants with enhanced tolerance or resistance to environmental stress conditions based on said new genes.

It is also an aim of the present invention to provide recombinant polynucleic acids comprising said new genes.

It is further an aim of the present invention to provide plant cells and plants transformed with said new genes.

It is further an aim of the present invention to provide plant cells and plants with enhanced tolerance or resistance to environmental stress conditions.

The present invention relates more particularly to a method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.

It has been found that the transfer of genes from plants which are often difficult to assay for certain characteristics, to lower eukaryotes, such as yeasts and fungi, but

in particular yeast, especially Saccharomyces, is relatively-easy to achieve, whereby it has now been shown that the results of testing for tolerance or resistance to environmental conditions in the resulting yeast cells gives a relatively reliable measure of the capability of the inserted coding sequence or gene to induce tolerance or resistance to environmental stress in plants. Thus the expression of polynucleic acid sequences comprising the gene or coding sequence which are responsible for inducing tolerance or resistance to environmental stress conditions can be enhanced in the plant species from which it originates or in any other plant species.

In the present context the term "enhancing" must be understood to mean that the levels of molecules correlated with stress protection in a transformed plant cell, plant tissue or plant part will be "substantially increased" or "elevated" meaning that this level will be greater than the levels in an untransformed plant.

This may be achieved by inducing overexpression of suitable genetic information which is already present, or by any other suitable means of introducing into the plant cell heterologous information resulting in a capability to tolerate or resist environmental stress.

The term "environmental stress" has been defined in different ways in the prior art and largely overlaps with the term "osmotic stress". Holmberg et al., 1998 for instance define different environmental stress factors which result in abiotic stress. Salinity, drought, heat, chilling and freezing are all described as examples of conditions which induce osmotic stress. The term "environmental stress" as used in the present invention refers to any adverse effect on metabolism, growth or viability of the cell, tissue, seed, organ or whole plant which is produced by an non-living or non-biological environmental stressor. More particularly, it also encompasses environmental factors such as water stress (flooding, drought, dehydration), anaerobic (low level of oxygen, CO_2 etc.), aerobic stress, osmotic stress, salt stress, temperature stress (hot/heat, cold, freezing, frost) or nutrients/pollutants stress.

The term "anaerobic stress" means any reduction in oxygen levels sufficient to produce a stress as hereinbefore defined, including hypoxia and anoxia.

The term "flooding stress" refers to any stress which is associated with or induced by prolonged or transient immersion of a plant, plant part, tissue or isolated cell in a liquid medium such as occurs during monsoon, wet season, flash flooding or excessive irrigation of plants, etc.

"Cold stress" and "heat stress" are stresses induced by temperatures which are respectively, below or above, the optimum range of growth temperatures for a

particular plant species. Such optimum growth temperature ranges are readily determined or known to those skilled in the art.

"Dehydration stress" is any stress which is associated with or induced by the loss of water, reduced turgor or reduced water content of a cell, tissue, organ or whole plant.

"Drought stress" refers to any stress which is induced by or associated with the deprivation of water or reduced supply of water to a cell, tissue, organ or organism.

"Oxidative stress" refers to any stress which increases the intracellular level of reactive oxygen species.

The terms "salinity-induced stress", "salt-stress" or similar term refer to any stress which is associated with or induced by elevated concentrations of salt and which result in a perturbation in the osmotic potential of the intracellular or extracellular environment of a cell.

Said salt can be for example, water soluble inorganic salts such as sodium sulfate, magnesium sulfate, calcium sulfate, sodium chloride, magnesium chloride, calcium chloride, potassium chloride etc., salts of agricultural fertilizers and salts associated with alkaline or acid soil conditions.

The transgenic plants obtained in accordance with the method of the present invention, upon the presence of the polynucleic acid and/or regulatory sequence introduced into said plant, attain resistance, tolerance or improved tolerance or resistance against environmental stress which the corresponding wild-type plant was susceptible to.

The terms "tolerance" and "resistance" cover the range of protection from a delay to complete inhibition of alteration in cellular metabolism, reduced cell growth and/or cell death caused by the environmental stress conditions defined herein before. Preferably, the transgenic plant obtained in accordance with the method of the present invention is tolerant or resistant to environmental stress conditions in the sense that said plant is capable of growing substantially normal under environmental conditions where the corresponding wild-type plant shows reduced growth, metabolism, viability, productivity and/or male or female sterility. Methodologies to determine plant growth or response to stress include, but are not limited to height measurements, leaf area, plant water relations, ability to flower, ability to generate progeny and yield or any other methodology known to those skilled in the art.

The terms "tolerance" and "resistance" may be used interchangeably in the present invention.

The methods according to the invention as set out below can be applied to any, higher plant, preferably important crops, preferably to all cells of a plant leading to an enhanced osmotic or any other form of environmental stress tolerance. By means of the embodiments as set out below, it now becomes possible to grow crops with improved yield, growth, development and productivity under environmental stress conditions, it may even become possible for instance to grow crops in areas where they cannot grow without the induced osmotolerance according to the invention.

In order to do a thorough screening for relevant plant genes and/or coding sequences, it is preferred to apply a method according to the invention whereby said cDNA library comprises copies of essentially all mRNA of said plant cell. Probably only coding sequences are sufficient. For the screening of genes involved in environmental stress, it is preferred to use a cDNA library from siliques (fruits, containing the maturing seeds), such as the siliques from *Arabidopsis*, because genes involved in for instance osmotolerance are preferentially expressed in these organs.

Although the genetic information may be introduced into yeast for screening by any suitable method, as long as it is in a functional format long enough tor testing of tolerance or resistance to environmental stress conditions, it is preferred for ease of operation to use a well known vector such as a 2μ plasmid. It is to be preferred to have the coding sequence or the gene under control of a strong constitutive yeast promoter, to enhance good expression of the gene or coding sequence of interest. Strong constitutive yeast promoters are well known in the art and include, but are not limited to the yeast TPI promoter.

The term "gene" as used herein refers to any DNA sequence comprising several operably linked DNA fragments such as a promoter and a 5' untranslated region (the 5'UTR), a coding region (which may or may not code for a protein), and an untranslated 3' region (3'UTR) comprising a polyadenylation site. Typically in plant cells, the 5'UTR, the coding region and the 3'UTR (together referred to as the transcribed DNA region) are transcribed into an RNA which, in the case of a protein encoding gene, is translated into a protein. A gene may include additional DNA fragments such as, for example, introns. As used herein, a genetic locus is the position of a given gene in the genome of a plant.

The present invention more particularly relates to an isolated polynucleic acid obtainable by a method comprising the preparation of a cDNA as set out above comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an

enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.

The term "polynucleic acid" refers to DNA or RNA, or amplified versions thereof, or the complement thereof.

The present invention more particularly provides an isolated polynucleic acid obtainable by a method as defined above which encodes a polypeptide as listed in Table 1.

The capacity of an isolated polynucleic acid to confer tolerance or resistance to environmental stress conditions can be tested according to methods well-known in the art, see for example, Grillo et al. (1996), Peassarakli et al. (Editor), Nilsen et al. (1996), Shinozaki et al. (1999), Jones et al. (1989), Fowden et al. (1993) or as described in the appended examples.

The present invention more particularly relates to an isolated polynucleic acid which encodes a homolog of any of the polypeptides as listed in Table 1, which is chosen from:

(a) any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, or 121, or the complementary strands thereof;
(b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
(c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b), or,
(d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

Said fragment as defined above are preferably unique fragments of said sequences.

The term "hybridizing" refers to hybridization conditions as described in Sambrook (1989), preferably specific or stringent hybridization conditions are aimed at.

Stringent conditions are sequence dependent and will be different in different circumstances. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength and pH. The Tm is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Typically, stringent conditions will be those in which the salt concentration is about 0.02 molar at pH 7 and the temperature is at least about 60°C.

In the present invention, genomic DNA or cDNA comprising the polynucleic acids of the invention can be identified in standard Southern blots under stringent conditions using the cDNA sequence shown. The preparation of both genomic and cDNA libraries is within the skill of the art. Examples of hybridization conditions are also given in the Examples section.

The present invention also relates to the isolated polynucleic acids which encode polypeptides which are a homolog of the polypeptides as set out in Table 1 useful for the production of plants which are resistant or tolerant to environmental stress conditions.

The present invention also relates to a polynucleic acid comprising at least part of any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121, or at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121. Preferably, said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 2, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76 or 78. Said part of said gene is preferably a unique part.

The present invention preferably relates to the use of a polynucleic acid comprising at least part of any of SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, or at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to any of

SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121 for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

Preferably, said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Said part of said gene is preferably a unique part.

The present invention particularly relates to an isolated polynucleic acid as defined above, which encodes a plant homolog of yeast DBF2 kinase, more particularly a DBF2 kinase homolog from Arabidopsis thaliana termed At-DBF2, which can at least be used to confer enhanced environmental stress tolerance or resistance in plants and yeast.

More preferably, the present invention relates to an isolated polynucleic acid encoding a plant DFB2 kinase, which is chosen from:

(a) SEQ ID NO 1, or the complementary strand thereof;
(b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
(e) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b), or,
(c) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

Alternatively, the present invention relates to a polynucleic acid derived from a plant comprising at least part of SEQ ID NO 1, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 1. Preferably said gene encodes a protein

having substantially the same biological activity as the protein having the sequence of SEQ ID NO 2.

The present invention also relates to the use of an isolated polynucleic acid as defined above which encodes a plant HSP 17.6A protein for the production of transgenic plants, more particularly a homolog from Arabidopsis thaliana, which at least can be used to confer enhanced environmental stress tolerance in plants and yeast.

More preferably, the present invention relates to the use of an isolated polynucleic acid as defined above which is chosen from:

(a) SEQ ID NO 3, or the complementary strand thereof;
(b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
(c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
(d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

The present invention also relates to the use of a polynucleic acid comprising at least part of SEQ ID NO 3, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 3. Preferably said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 4, for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

More preferably, the present invention relates to the use of an isolated polynucleic acid as defined above which is chosen from:

(a) any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or the complementary strand thereof;

(b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
(c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
(d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

The present invention preferably relates to the use of a polynucleic acid comprising at least part of any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

Preferably, said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Said part of said gene is preferably a unique part.

According to another preferred embodiment, the present invention relates to an isolated polynucleic acid as defined above, which encodes a protein termed c74, more particularly a plant homolog of c74, even more preferably a c74 from Arabidopsis thaliana, which at least can be used to confer enhanced environmental stress tolerance in plants and yeast.

More particularly, the present invention relates to an isolated polynucleic acid as defined above, which is chosen from:

(a) SEQ ID NO 5, or the complementary strand thereof;
(b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;

(c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,

(d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

The present invention also relates to a polynucleic acid comprising at least part of SEQ ID NO 5, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 5. Preferably said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 6.

Two nucleic acid sequences or polypeptides are said to be "identical" according to the present invention if the sequence of nucleotides or amino acid residues, respectively, in the two sequences is the same when aligned for maximum correspondence as described below. The term "complementary to" is used herein to mean that the complementary sequence hybridizes to all or a portion of a given polynucleotide sequence.

Sequence comparisons between two (or more) polynucleic acid or polypeptide sequences are typically performed by comparing sequences of the two sequences over a "comparison window" to identify and compare local regions of sequence similarity. A "comparison window", as used herein, refers to a segment of at least about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman (1981), by the homology alignment algorithm of Needleman and Wunsch (1970), by the search for similarity method of Pearson and Lipman (1988), by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by visual inspection.

"Percentage of sequence identity" is determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleic acid or polypeptide sequences in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity.

The term "substantial identity" of polynucleic acid or polypeptide sequences means that a polynucleotide sequence comprises a sequence that has at least 60%, 65%, 70% or 75% sequence identity, preferably at least 80% or 85%, more preferably at least 90% and most preferably at least 95 %, compared to a reference sequence using the programs described above (preferably BLAST) using standard parameters. One of skill will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like. Substantial identity of amino acid sequences for these purposes normally means sequence identity of at least 40%, 45%, 50% or 55% preferably at least 60%, 65%, 70%, 75%, 80% or 85% more preferably at least 90%, and most preferably at least 95%. Polypeptides which are "substantially similar" share sequences as noted above except that residue positions which are not identical may differ by conservative amino acid changes. Conservative amino acid substitutions refer to the interchangeability of residues having similar side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, and asparagine-glutamine.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other, or a third nucleic acid, under stringent conditions.

More particularly, the polynucleic acids as used herein will comprise at least part of a DNA sequence which is essentially similar, or, preferentially, essentially identical or identical to one or both of the nucleotide or amino acid sequences corresponding to SEQ ID NO 1 to 121 disclosed herein, more specifically in the nucleotide sequence encoding, or the amino-acid sequence corresponding to the "active domain" of the respective protein or polypeptide.

The polynucleic acid sequences according to the present invention can be produced by means of any nucleic acid amplification technique known in the art such as PCR or conventional chemical synthesis.

For a general overview of PCR see PCR Protocols (Innis et al. (1990)).

Polynucleotides may also be synthesized by well-known techniques as described in the technical literature. See, e.g., Carruthers et al. (1982) and Adams et al. (1983). Double stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the strands together under appropriate conditions, or by adding the complementary strand using DNA polymerase with an appropriate primer sequence.

The present invention more particularly relates to an isolated polypeptide encoded by a polynucleic acid according to any of the polynucleic acids as defined above, or a functional fragment thereof.

The present invention preferably relates to an isolated polypeptide as listed in Table 1 or to an isolated polypeptide encoded by a polynucleic acid isolated as defined above. Preferably, the present invention relates to polypeptides or peptides having at least part of the sequence of any of SEQ ID NO NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Preferably, said part is a unique part and preferably includes the active domain of said polypeptide. Preferably said polypeptide is a recombinant polypeptide.

The term "isolated" distinguishes the protein or polynucleic acid according to the invention from the naturally occuring one.

The present invention also relates to a polypeptide comprising at least part of a polypeptide which is at least 50%, 55%, 60%, 65% identical, preferentially at least 70%, 75% identical, more preferably at least 80% or 85% identical, and most

preferably at least 90% or 95% identical to any of SEQ ID NO NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120.

The terms "polypeptide" and "protein" are used interchangeably throughout the present description.

Said polypeptide preferably has the ability to confer tolerance or resistance to environmental stress conditions in at least plants, plant parts, plant tissues, plant cells, plant calli or yeast.

The term "functional fragment" refers to a fragment having substantially the biological activity of the protein from which it is derived.

The polypeptides of the present invention may be produced by recombinant expression in prokaryotic and eukaryotic engineered cells such as bacteria, yeast or fungi. It is expected that those of skill in the art are knowledgeable in the numerous expression systems available for expression in these systems.

The present invention more particularly relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising transiently introducing into a plant cell a recombinant DNA comprising any of the polynucleic acids as defined above which when (over)expressed in a plant cell enhances tolerance or resistance to environmental stress of said plant.

The term "plant cell" as defined above also comprises plant tissue or a plant as a whole. The present invention more particularly relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising transiently introducing into a plant cell a recombinant DNA comprising any of the polynucleic acids encoding a protein as listed in Table 1 which when (over)expressed in a plant cell enhances tolerance or resistance to environmental stress in said plant.

The term "(over)expression" refers to the fact that the polypeptides of the invention encoded by said polynucleic acid are preferably expressed in an amount effective to confer tolerance or resistance to the transformed plant, to an amount of salt, heat, cold, (or other stress factors) that inhibits the growth of the corresponding untransformed plant.

Several methods to obtain transient introduction and expression of a recombinant DNA in a plant are known to the art. For example, plant virus vectors can

be used to obtain such purpose. Examples conferring to the use of plant viral vectors are described in Porta and Lomonossoff (1996), WO9320217 and US 5,589,367.

The present invention also relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising stably introducing into the genome of a plant cell a recombinant DNA comprising any of the polynucleic acids as defined above which when (over)expressed in a plant cell enhances the environmental stress tolerance or resistance of a plant.

The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress conditions, said method comprising introducing into the genome of a plant cell a recombinant DNA comprising any of the polynucleic acids encoding a protein as listed Table 1 which when (over)expressed in a plant cell enhances the environmental stress resistance of said plant.

According to a preferred embodiment, the present invention relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding a DBF2 kinase, preferably a plant DBF2 kinase, most preferably an Arabidopsis DBF2 kinase.

According to another preferred embodiment, the present invention relates to a method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding an HSP 17.6A protein, preferably a plant HSP 17.6A protein, most preferably an Arabidopsis HSP 17.6A.

According to a preferred embodiment, the present invention relates to a method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding a c74 protein, preferably a plant c74 protein, most preferably a Arabidopsis c74 protein.

Preferably, the present invention relates to a method as defined above, comprising:

(a) introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:
   - a polynucleic acid as defined above, and,
   - a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit

and under the control of said plant-expressible promoter, and,

(b) regenerating said plant from said plant cell.

The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising indirectly increasing of inducing the expression of an endogenous gene in said plant comprised within a polynucleic acid as defined above or indirectly increasing of inducing te activity of a protein as defined above.

The present invention also relates to a method as defined above, comprising:

(a) introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:
  - a DNA encoding a protein which when expressed in said plant cell at an effective amount indirectly increases or induces the expression of an endogenous polynucleic acid or indirectly increases or induces the protein activity of a protein encoded by said polynucleic acid of the present invention, and,
  - a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter, and,

(b) regenerating said plant from said plant cell.

A "recombinant" DNA molecule will comprise a "heterologous sequence" meaning that said recombinant DNA molecule will comprise a sequence originating from a foreign species, or, if from the same species, may be substantially modified from its original form. For example, a promoter operably linked to a structural gene which is from a species different from which the structural gene was derived, or, if from the same species, may be substantially modified from its original form.

The present invention also relates to a method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress conditions, said method comprising indirectly increasing or inducing the expression of an endogenous gene in said plant comprised within a polynucleic acid as defined above or indirectly increasing or inducing the activity of a protein of the invention as defined above. According to this embodiment, other polynucleic acids modulating the expression or the activity of a protein according to the present invention may be introduced

transiently or stably into the genome of said plants. The term “modulating” means enhancing, inducing, increasing, decreasing or inhibiting.

Increase or induction of expression or induction or increase of protein activity is required when said regulator protein is a positive regulator of the expression or the activity of at least one of the polynucleic acids or protein of the present invention.

Decrease or inhibition of expression or decrease or inhibition of protein activity is required when said regulator protein is a negative regulator of the expression or activity of at least one of the polynucleic acids or proteins of the present invention.

Increase of the activity of said polypeptide according to the present invention is obtained, according to one embodiment of the invention, by influencing endogenous gene expression in the plant. This is preferably achieved by the introduction of one or more polynucleic acid sequences according to the invention into the plant genome, in a suitable conformation for gene expression (e.g. under control of a plant-expressible promoter). This will result in increased or induced expression (overexpression) or increased or induced activity of the protein in the plant cells, and, in the presence of an adequate substrate, in an increase of tolerance or resistance to environmental stress conditions in a transgenic plant or plant cell as compared to a non-transgenic plant or plant cell. This increase in tolerance can be measured by measuring mRNA levels, or where appropriate, the level or activity of the respective protein (e.g. by means of ELISA, activity of the enzyme as measured by any technique known in the art). Endogenous gene expression refers to the expression of a protein which is naturally found in the plant, plant part or plant cell concerned.

Alternatively, said enhanced tolerance or resistance to environmental stress conditions may be achieved by introducing into the genome of the plant, one or more transgenes which interact with the expression of endogenous genes (polynucleic acids) according to the present invention, by anti-sense RNA, co-suppression or ribozyme suppression of genes which normally inhibit the expression of the polynucleic acids of the present invention or by suppression of genes which normally inhibit the activity of the polypeptides of the invention as defined above.

For inhibition of expression, the nucleic acid segment to be introduced generally will be substantially identical to at least a portion of the endogenous gene or genes to be repressed. The sequence, however, need not be perfectly identical to inhibit expression. The vectors of the present invention can be designed such that the inhibitory effect applies to other genes within a family of genes exhibiting homology or substantial homology to the target gene.

For antisense suppression, the introduced sequence also need not be full length relative to either the primary transcription product or fully processed mRNA.

Generally, higher homology can be used to compensate for the use of a shorter sequence.

Furthermore, the introduced sequence need not have the same intron or exon pattern, and homology of non-coding segments may be equally effective. Normally, a sequence of between about 30 or 40 nucleotides up to the full length sequence should be used, though a sequence of at least about 100 nucleotides is preferred, a sequence of at least about 200 nucleotides is more preferred, and a sequence of about 500 to about 1700 nucleotides is especially preferred.

Catalytic RNA molecules or ribozymes can also be used to inhibit expression of genes as explained above. It is possible to design ribozymes that specifically pair with virtually any target RNA and cleave the phosphodiester backbone at a specific location, thereby functionally inactivating the target RNA. In carrying out this cleavage, the ribozyme is not itself altered, and is thus capable of recycling and cleaving other molecules, making it a true enzyme. The inclusion of ribozyme sequences within antisense RNAs confers RNA-cleaving activity upon them, thereby increasing the activity of the constructs.

A number of classes of ribozymes have been identified. One class of ribozymes is derived from a number of small circular RNAs which are capable of selfcleavage and replication in plants. The RNAs replicate either alone (viroid RNAs) or with a helper virus (satellite RNAs). Examples include RNAs from avocado sunblotch viroid and the satellite RNAs from tobacco ringspot virus, lucerne transient streak virus, velvet tobacco mottle virus, solanum nodiflorum mottle virus and subterranean clover mottle virus. The design and use of target RNA-specific ribozymes is described in Haseloff et al. (1988).

Another method of suppression of gene expression is sense suppression. Introduction of nucleic acid configured in the sense orientation has been shown to be an effective means by which to block the transcription of target genes. For an example of the use of this method to modulate expression of endogenous genes see, Napoli et al. (1990), and U.S. Patents Nos. 5,034,323, 5,231,020, and 5,283,184.

The suppressive effect may occur where the introduced sequence contains no coding sequence per se, but only intron or untranslated sequences homologous to sequences present in the primary transcript of the endogenous sequence. The introduced sequence generally will be substantially identical to the endogenous

sequence intended to be repressed. This minimal identity will typically be greater than about 65%, but a higher identity might exert a more effective repression of expression of the endogenous sequences. Substantially greater identity of more than about 80% is preferred, though about 95% to absolute identity would be most preferred. As with antisense regulation, the effect should apply to any other proteins within a similar family of genes exhibiting homology or substantial homology.

For sense suppression, the introduced sequence, needing less than absolute identity, also need not be full length, relative to either the primary transcription product or fully processed mRNA. This may be preferred to avoid concurrent production of some plants which are overexpressers. A higher identity in a shorter than full length sequence compensates for a longer, less identical sequence. Furthermore, the introduced sequence need not have the same intron or exon pattern, and identity of non-coding segments will be equally effective. Normally, a sequence of the size ranges noted above for antisense regulation is used.

Other methods for altering or replacing genes known in the art can also be used to inhibit expression of a gene. For instance, insertional mutants using T-DNA or transposons can be generated. See, e.g., Haring et al. (1991) and Walbot (1992). Another strategy in genetic engineering of plants and animals is targeted gene replacement. Homologous recombination has typically been used for this purpose (see, Capecchi (1989)).

Alternatively, the present invention also relates to a method as defined above wherein said DNA encodes a sense or antisense RNA or a ribozyme capable of indirectly increasing or inducing the expression of an endogenous polynucleic acid sequence according to the invention as defined above or increasing or inducing the activity of a protein of the invention as defined above. Preferably said endogenous polynucleic acid encodes a protein as listed in Table 1.

The present invention also relates to a recombinant polynucleic acid comprising: a polynucleic acid as defined above, and, a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control of said plant-expressible promoter.

The present invention also relates to a recombinant polynucleic acid comprising:

(a) a DNA encoding a protein which when expressed in said plant at an effective amount indirectly increases or induces the expression of an endogenous

polynucleic acid as defined above or indirectly increases or induces the protein activity of a polypeptide as defined above, and,

(b) a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.

An "endogenous" polynucleic acid refers to a polynucleic acid that is already present in the plant species before transformation.

Said recombinant polynucleic acid as described here above is generally also referred to as a "recombinant vector" or an "expression cassette". An expression cassette of the invention can be cloned into an expression vector by standard methods. The expression vector can then be introduced into host cells by currently available DNA transfer methods.

The present invention also relates to the recombinant polynucleic acid as defined above, comprising a DNA which encodes an anti-sense RNA, a ribozyme or a sense RNA which increases or induces the activity of a protein as defined above in said cell. Preferably said protein is listed in Table 1.

More particularly, the present invention relates to a recombinant polynucleic acid comprising at least part of the nucleotide sequence of any of SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121.

Preferably, the present invention relates to a recombinant polynucleic acid comprising at least part of the coding sequence of a gene encoding a protein as listed in Table 1. Preferably, said "part" is a unique part of any of said nucleotide sequences. (26-28) As used herein, the term a "plant-expressible promoter" refers to a promoter that is capable of driving transcription in a plant cell. This includes any promoter of plant origin, including the natural promoter of the transcribed DNA sequence, but also any promoter of non-plant origin which is capable of directing transcription in a plant cell. The promoter may also be an artificial or synthetic promoter. The term "plant-expressible promoter" includes, but is not restricted to, constitutive, inducible, organ-, tissue-specific or developmentally regulated promoters.

According to the invention, production and/or activity of a polypeptide according to the present invention in a plant or in plant parts is increased by introducing *one or more* polynucleic acids according to the invention into the genome of the plant. More specifically, the constitutive promoter can be, but is not restricted to, one of the following: a 35S promoter (Odell et al. (1985)), a 35S'3 promoter (Hull and Howell

(1987)), the promoter of the nopaline synthase gene ("PNOS") of the Ti-plasmid (Herrera -Estrella, (1983)) or the promoter of the octopine synthase gene ("POCS", De Greve et al. (1982)). It is clear that other constitutive promoters can be used to obtain similar effects. A list of plant-expressible promoters that can be used according to the present invention is given in Table 2.

For specific embodiments of this invention, the use of inducible promoters can provide certain advantages. Modulation of protein levels or protein activity may be required in certain parts of the plant, making it possible to limit modulation to a certain period of culture or developmental stage of the plant.

For specific embodiments of this invention, the use of organ- or tissue-specific or chemical inducible promoters can provide certain advantages. Thus, in specific embodiments of the invention, the gene(s) or part thereof is (are) placed under the control of a promoter directing expression in specific plant tissues or organs, such as for instance roots, leaves, harvestable parts, etc.

It is also possible to use a promoter that can be induced upon the environmental stress conditions. Such promoters can be taken for example from stress-related genes which are regulated directly by an environmental, i.e. preferable abiotic, stress in a plant cell, including genes for which expression is increased, reduced or otherwise altered. These stress related genes comprise genes the expression of which is either induced or repressed by anaerobic stress, flooding stress, cold stress, dehydration stress, drought stress, heat stress or salinity. An exemplary list of such promoters is given in Table 3.

The recombinant polynucleic acids according to the present invention may include further regulatory or other sequences from other genes, such as leader sequences (e.g. the cab22 leader from Petunia), 3' transcription termination and polyadenylation signals (e.g. from the octopine synthase gene or the nopaline synthase gene), plant translation initiation consensus sequences, introns, transcription enhancers and other regulatory elements such as adh intron 1, etc, which is or are operably linked to the gene or a fragment thereof. Additionally, the recombinant polynucleic acid can be constructed and employed to target the gene product of the polynucleic acid of the invention to a specific intracellular compartment within a plant cell on to direct a protein to the extracellular environment. This can generally be obtained by operably joining a DNA sequence encoding a transit or signal peptide to the recombinant polynucleic acid.

The recombinant DNA comprising one or more polynucleic acids according to the present invention may be accompanied by a chimeric marker gene (Hansen et al., 1999 and references therein). The chimeric marker gene can comprise a marker DNA that is operably linked at its 5' end to a plant-expressible promoter, preferably a constitutive promoter, such as the CaMV 35S promoter, or a light inducible promoter such as the promoter of the gene encoding the small subunit of Rubisco; and operably linked at its 3' end to suitable plant transcription 3' end formation and polyadenylation signals. It is expected that the choice of the marker DNA is not critical, and any suitable marker DNA can be used. For example, a marker DNA can encode a protein that provides a distinguishable color to the transformed plant cell, such as the A1 gene (Meyer et al., (1987)), can provide herbicide resistance to the transformed plant cell, such as the *bar* gene, encoding resistance to phosphinothricin (EP 0 242 246), or can provide antibiotic resistance to the transformed cells, such as the *aac(6')* gene, encoding resistance to gentamycin (WO94/01560).

According to another embodiment, the present invention invention relates to the use of the polynucleic acids above as selectable marker gene. More preferably, the present invention also relates to the use of the plant DBF2 gene as defined above as selectable marker gene, selection taking place with treatment with a stress condition.

The recombinant DNA vectors according to the present invention comprising the sequences from genes of the invention will typically also comprise a marker gene which confers a selectable phenotype on plant cells. For example, the marker may encode biocide resistance, particularly antibiotic resistance, such as resistance to kanamycin, G418, bleomycin, hygromycin, or herbicide resistance, such as resistance to chlorosulforon or Basta.

The present invention also relates to a recombinant host cell transformed with an isolated polynucleic acid as defined above. Said host can be any host known in the art. Preferably said recombinant host cell is a plant cell, yeast, fungi, insect cell, etc. In order to be efficiently expressed in said host, said polynucleic acids can be combined with any promoter known to function in said host system. Methods for transforming said host cells are also well known in the art.

The present invention particularly also relates to a plant cell transformed with at least one recombinant polynucleic acid as defined above.

The present invention also relates to a plant consisting essentially of plant cells transformed with at least one recombinant polynucleic acid as defined above.

A "transgenic plant" refers to a plant comprising a transgene in the genome of essentially all of its cells.

DNA constructs of the invention may be introduced into the genome of the desired plant host by a variety of conventional techniques (see for example Hansen et al., 1999 for review and WO 99/05902). For example, DNA constructs of the invention may be introduced into the genome of the desired plant host by using techniques such as protoplast transformation, biolistics or microprojectile bombardment or Agrobacterium mediated transformation.

Microinjection techniques are known in the art and well described in the scientific and patent literature. The introduction of DNA constructs using polyethylene glycol precipitation is described in Paszkowski et al. (1984).

Electroporation techniques are described in Fromm et al. (1985). Biolistic transformation techniques are described in Klein et al. (1987).

Alternatively, the DNA constructs may be combined with suitable T-DNA flanking regions and introduced into a conventional Agrobacterium host vector. The virulence functions of the Agrobacterium host will direct the insertion of the construct and adjacent marker into the plant cell DNA when the cell is infected by the bacteria. Agrobacterium tumefaciens-mediated transformation techniques, including disarming and use of binary vectors, are well described in the scientific literature. See, for example Horsch et al. (1984), and Fraley et al. (1983).

Transformed plant cells which are derived by any of the above transformation techniques can be cultured to regenerate a whole plant which possesses the transformed genotype and thus the desired phenotype. Such regeneration techniques rely on manipulation of certain phytohormones in a tissue culture growth medium. Plant regeneration from cultured protoplasts is described in Evans et al. (1983); and Binding (1985). Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are described generally in Klee et al. (1987).

The polynucleic acids and polypeptides of the invention can be used to confer desired traits on a broad range of plants, including monocotyledonous or dicotyledonous plants, preferably they belong to a plant species of interest in agriculture, wood culture or horticulture, such as a crop plant, root plant, oil producing plant, wood producing plant, fruit producing plant, fodder or forage legume, companion or ornamental or horticultured plant. The plants can include species from the genera Actinidia, Apium, Allium, Ananas, Arachis, Arisaema, Asparagus, Atropa, Avena, Beta,

Brassica, Carica, Cichorium, Citrus, Citrullus, Capsicum, Cucumis, Cucurbita, Cydonia, Daucus, Diospyros, Fragaria, Glycine, Gossypium, Helianthus, Heterocallis, Hordeum, Hyoscyamus, Ipomoea, Lactuca, Linum, Lolium, Lycopersicon, Malus, Mangifera, Manihot, Majorana, Medicago, Musa, Nicotiana, Oryza, Panicum, Pannesetum, Persea, Petroselinum, Phaseolus, Pisum, Pyrus, Prunus, Raphanus, Rheum, Ribes, Rubus, Saccharum, Secale, Senecio, Sinapis, Solanum, Sorghum, Spinacia, Trigonella, Triticum, Vaccinium, Vitis, Vigna, Zea, and Zingiber. Additional species are not excluded. Crops grown on cultivated lands in arid and semi-arid areas in which irrigation with ground water is needed may advantageously benefit from the invention.

One of skill will recognize that after the recombinant polynucleic acid is stably incorporated in transgenic plants and confirmed to be operable, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed. As described before, the plant cells, plant tissue, in particular, transgenic plants of the invention display a certain higher or enhanced degree of tolerance (or even resistance) to environmental stress conditions compared to the corresponding wild-type plants. For the meaning of "environmental stress", see supra. In a preferred embodiment of the present invention, the transgenic plant displays increased tolerance to osmotic stress, salt stress, cold and/or heat stress. An increase in tolerance to such environmental stress is understood to refer to a tolerance to a level of such stress which inhibits the growth and productivity of the corresponding untransformed plant, as determined by methodologies known to the art. Such increased tolerance in transgenic plants is related to an increased expression level in the transgenic plant or parts thereof of one ore more of the polynucleic acids of the present invention and/or to an increased level of activity of the polypeptide(s) encoded by said polynucleic acid, as determined by methodologies known to the art. In comparison with their untransformed counterparts, and determined according to methodologies known in the art, a transgenic plant according to the present invention shows an increased growth, viability, metabolism, fertility and/or productivity under mild environmental stress conditions. In the alternative, a transgenic plant according to the invention can grow under environmental stress conditions wherein the untransformed counterparts can not grow. An increase in tolerance to salt stress is understood to refer to the capability of the transgenic plant to grow under stress conditions which inhibit the growth of at least 95% of the parent, non-stress tolerant plants from which the stress tolerant transgenic

plants are derived. Typically, the growth rate of stress tolerant plants of the invention will be inhibited by less than 50%, preferably less than 30%, and most preferably will have a growth rate which is not significantly inhibited by growth conditions which inhibit the growth of at least 95% of the parental, non-stress tolerant plants. In an alternative example, under mild environmental stress conditions, the growth and/or productivity of the transgenic plants is statistically at least 1 % higher than for their untransformed counterparts, preferably more than 5 % higher and most preferably more than 10 % higher.

Any transformed plant obtained according to the invention can be used in a conventional breeding scheme or in *in vitro* plant propagation to produce more transformed plants with the same characteristics and/or can be used to introduce the same characteristic in other varieties of the same or related species.

Furthermore, the characteristic of the transgenic plants of the present invention to maintain normal/rapid/high growth rates under environmental stress conditions can be combined with various approaches to confer environmental stress tolerance with the use of other stress tolerance genes. Some examples of such stress tolerant genes are provided in Holmberg and Bülow (1998). Most prior art approaches which include the introduction of various stress tolerance genes have the drawback that they result in reduced or abnormal growth (compared to non-transgenic controls) under normal, non-stressed conditions, namely stress tolerance comes at the expense of growth and productivity (Kasuga et al., 1999). This correlation between constitutive expression of stress-responsive genes and reduced growth rates under normal growth conditions indicates the presence of cross talk mechanisms between stress response control and growth control.

Furthermore, the characteristic of the transgenic plants of the present invention to display tolerance to environmental stress conditions can be combined with various approaches to confer to plants other stress tolerance genes, e.g., osmotic protectants such as mannitol, proline; glycine-betaine, water-channeling proteins, etc. Thus, the approach of the present invention to confer tolerance to environmental stress conditions to plants can be combined with prior art approaches which include introduction of various stress tolerance genes. Combination of these approaches may have additive and/or synergistic effects in enhancing tolerance or resistance to environmental stress.

Thus, it is immediately evident to the person skilled in the art that the method of the present invention can be employed to produce transgenic stress tolerant plant with

any further desired trait (see for review TIPTEC Plant Product & Crop Biotechnology 13 (1995), 312-397) comprising:

- (i) herbicide tolerance (DE-A 3701623; Stalker (1988)),
- (ii) insect resistance (Vaek (1987)),
- (iii) virus resistance (Powell (1986), Pappu (1995), Lawson (1996)),
- (iv) ozone resistance (Van Camp (1994)),
- (v) improving the preserving of fruits (Oeller (1991)),
- (vi) improvement of starch composition and/or production (Stark (1992), Visser (1991)),
- (vii) altering lipid composition (Voelker (1992)),
- (viii) production of (bio)polymers (Poirer (1992)),
- (ix) alteration of the flower color, e.g., bu manipulating the anthocyanin and flavonoid biosynthetic pathway (Meyer (1987), WO90/12084),
- (x) resistance to bacteria, insects and fungi (Duering (1996), Strittmatter (1995), Estruch (1997)),
- (xi) alteration of alkaloid and/or cardia glycoside composition,
- (xii) inducing maintaining male and/or female sterility (EP-A1 0 412 006; EP-A1 0 223 399; WO93/25695);
- (xiii) higher longevity of the inflorescences/flowers, and
- (xvi) stress resistance.

Thus, the present invention relates to any plant cell, plant tissue, or plant which due to genetic engineering displays an enhanced tolerance or resistance to environmental stress obtainable in accordance with the method of the present invention and comprising a further nucleic acid molecule conferring a novel phenotype to the plant such as one of those described above.

The present invention also relates to a callus or calli consisting essentially of plant cells as defined here above. Such transgenic calli can be preferably used for the production of secondary metabolites in plant cell suspension cultures.

The present invention also relates to any other harvestable part, organ or tissue or propagation material of the plant as defined here above.

The present invention also relates to the seed of a transgenic plant as defined here above, comprising said recombinant DNA.

The present invention also relates to the use of any isolated polynucleic acid as defined above to produce transgenic plants.

The present invention also relates to the use of a recombinant polynucleic acid as defined above, to produce transgenic plants, preferably transgenic plants having an enhanced tolerance or resistance to environmental stress conditions. Preferably said polynucleic acid encodes a polypeptide as listed in Table 1.

The present invention also relates to the use of an isolated polynucleic acid as defined above, to produce transgenic callus having an enhanced tolerance or resistance to environmental stress conditions. Preferably said polynucleic acid encodes a polypeptide as listed in Table 1.

The present invention also relates to probes and primers derived from the genes of the invention that are useful for instance for the isolation of additional genes having sequences which are similar to but differ from any of SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, but which encode a protein having substantially the same biological activity as a protein having the amino acids sequence of any of SEQ ID NO 2 to 120 (even numbers) by techniques known in the art, such as PCR. The presence of a homologous gene in another plant species can for instance be verified by means of Northern of Southern blotting experiments.

The present invention also relates to the cloning of the genomic counterpart of any of the cDNA sequences as represented in SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121. These genomic counterparts can be selected from a genomic library using these cDNA sequences as a probe. The present invention also relates to the coding region as well as the promoter region of any of said genomic clones.

The term "probe" according to the present invention refers to a single-stranded oligonucleotide *sequence* which is designed to specifically hybridize to any of the polynucleic acids of the invention.

The term "primer" refers to a single stranded oligonucleotide sequence capable of acting as a point of initiation for synthesis of a primer extension product which is complementary to the nucleic acid strand to be copied. Preferably the primer is about 5-50 nucleotides long. The term "target region" of a probe or a primer according to the present invention is a sequence within the polynucleic acid(s) to which the probe or the primer is completely complementary or partially complementary (i.e. with some degree

of mismatch). It is to be understood that the complement of said target sequence is also a suitable target sequence in some cases.

"Specific hybridization" of a probe to a target region of the polynucleic acid(s) means that the probe forms a duplex with part of this region or with the entire region under the experimental conditions used, and that under those conditions this probe does substantially not form a duplex with other regions of the polynucleic acids present in the sample to be analysed.

"Specific hybridization" of a primer to a target region of the polynucleic acid(s) means that, during the amplification step, said primer forms a duplex with part of this region or with the entire region under the experimental conditions used, and that under those conditions the primer does not form a duplex with other regions of the polynucleic acids present in the sample to be analysed. It is to be understood that "duplex" as used hereby, means a duplex that will lead to specific amplification.

Preferably, the probes of the invention are about 5 nucleotides to about 1 Kb long, more preferably from about 10 to 25 nucleotides. The nucleotides as used in the present invention may be ribonucleotides, deoxyribonucleotides and modified nucleotides such as inosine or nucleotides containing modified groups which do not essentially alter their hybridization characteristics. The probes according to the present invention preferably include parts of the cDNA sequences of any of the polynucleic acids as defined above.

The present invention also relates to a composition comprising a polynucleic acid sequence as defined above, a polypeptide as defined above, a probe as defined above or a primer as defined above.

The present invention also relates to a pharmaceutical or agrochemical composition comprising said polynucleic acid, a polypeptide of the invention as defined above.

The present invention also relates to antibodies specifically reacting with a protein or polypeptide according to the present invention.

The following Examples describe by way of example the tolerance and/or resistance to several environmental stress conditions observed for transgenic plants and yeast overexpressing some of the polynucleic acids according to the present invention. Unless stated otherwise in the Examples, all recombinant DNA techniques are carried out according to standard protocols as described in Sambrook et al. (1989) and in volumes 1 and 2 of Ausubel et al. (1994). Standard materials and methods for plant molecular work are described in Plant Molecular Biology Labfax (1993) by R.D.D.

Croy, jointly published by BIOS Scientific Publications Ltd. (UK) and Blackwell Scientific Publications, UK.

These examples and figures are not to be construed as limiting to any of the embodiments of the present invention as set out above. All of the references mentioned herein are incorporated by reference.

BRIEF DESCRIPTION OF THE FIGURES AND TABLES

Figure 1. *At-DBF2* encodes a functional homolog of the yeast Dbf2 (A) Comparison of the deduced amino acid sequence of *At-DBF2* with that of yeast *DBF2*. Gaps were introduced to optimize the alignment. Roman numerals above the At-DBF2 sequence indicate the protein kinase catalytic subdomains defined by Hanks et al. (1988). (B) Complementation of *dbf2*. The *dbf2* mutant S7-4A [*MATa dbf2Δ*::URA3 *ura3 leu2 ade5 trp1 his7*] (Toyn and Johnston, 1994) (B1) forms swollen pairs of daughter cells (dumbbells) at restrictive temperature (37^0 C). The defective morphology of the *dbf2* mutant can be complemented by transformation with the pYX112 centromeric plasmid (Ingenius, R&D system) containing the *At-DBF2* cDNA (B2) or *DBF2* (B3); wild type (CG378 strain, *MATa ade5 leu2 trp1 ura3*) (B4). Log phase cultures were shifted from 28°C to 37°C and photographed after 16 hours. After 16 hours, 98% of the S7-4A cells arrested with a dumbbell morphology (B1) whereas 6,1 and 0% of dumbbells were observed in B1, B3 and B4. Strains were kindly provided by (Dr Lindl, Max Planck Institut fur Zuchtungsforschung, Koln, Germany).

Figure 2. Overexpression of *DBF2* or *At-DBF2* enhances tolerance to osmotic, salt, heat and cold stress. Yeast cells were grown in YPD and cell density was adjusted to OD600 at 2. (1) DY, (2) DY transformed with pYX212 containing *DBF2,* pYX-YDBF2 , (3) DY transformed with vector alone or (4) with vector containing *At-DBF2,* pYX-AtDBF2. Serial dilutions were made in step1:10. Ten µl of each dilution was spotted on solid YPD medium (control) supplemented with 2M sorbitol (osmotic stress) or 1.2 M NaCl (salt stress) or 4µl H_2O_2 (oxidative stress) and incubated at 28^0C or at 42^0C (heat stress) or at 4^0C (cold stress) for 3 days.

Figure 3. *DBF2* and *At-DBF2* are induced by stress. (a) Northern analysis showing the kinetics of *At-DBF2* induction in plants treated with PEG 6000 20 % and the one of *DBF2* in yeast treated with sorbitol 2M for the time indicated. (b) Northern analysis *of At-DBF2* in 10 day-old-plants grown for 5 hours in control conditions (as described in Verbruggen et al. 1993) (1), at 37^0C (2), with PEG 6000 20 % (3), NaCl 1% (4), at 4^0C (5) or with 0.4 mM H_2O_2 (6); and of *DBF2* in yeast cells grown for 11/2 hour in YPD (1), at 37^0C (2), with sorbitol 2M (3), with NaCl 1.2 M (4), at 4^0C (5) or with 0.4 mM H_2O_2 (6). Control of loading has been done with EtBr staining and is shown under each Northern analysis.

(c) Western analysis of At-DBF2 in Arabidopsis. Samples are similar to those analysed in (b). Antibodies used were raised against yeast Dbf2 and kindly provided by Dr L. Leindl (Max Planck Institut fur Zuchtungsforschung, Koln, Germany).

Figure 4. *DBF2* overexpression can suppress *hog1* osmosensitivity. The *hog1* mutant (4) [W303-1A, *MATa*, *hog1Δ:: TRP1*] and wild type (W303) (1) were kindly provided by Dr Thevelein (Katholieke Universiteit Leuven, Belgium). The *hog1* mutant was transformed with pYX-YDBF2 (2) or pYX-AtDBF2 (3). Each of the 4 strains was grown for 16 hours in YPD (rich medium), and cell density was adjusted to OD600 at 2. Serial dilutions, 1:10 were made at five consecutive steps. Ten microliter of each dilution was spotted on solid YPD medium (control) or solid YPD medium supplemented with 0,9 M NaCl and incubated at 28°C for 3 days.

Figure 5. *T-DBF2* (*Nicotiana tabacum* DBF2) is periodically expressed during plant cell cycle. Tobacco *DBF2* expression has been followed in BY2 cells synchronised with aphidicolin (a & b) or with propyzamide (c & d) with *At-DBF2* as probe. The measure of relative rate of DNA synthesis and of the mitotic index, the use of the cell cycle markers *CYCB1.2* and *H4* markers have been previously described (Reicheld et al., 1995). *T-DB*F2 transcript levels were quantified from the blots shown in b and d using a PhosphorImager (Molecular Dynamics).

Figure 6. shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left section) upon applying a salt stress of 200 mM NaCl overnight.

Figure 7 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left section) upon applying an osmotic stress induced by 20% PEG overnight.

Figure 8 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left

section) upon applying a cold stress by gradually decreasing the temperature untill –7°C.

Figure 9 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left section) upon applying a heat stress of 2 hours at 48°C.

Figure 10 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left section). It can be concluded that the P35S-At-DBF2 transformed plants do not show morphological abnormalities compared to the control transgenic plants.

Figure 11 shows the results of a salt stress tolerance test with transgenic *A. thaliana* plants overexpressing HSP 17.6A (A) or c74 (B). The control plants (bottom left in A en B) is a transgenic line tranformed with pBIN-35S-CaMVter. The other sections in A are 5 independently obtained transgenic lines overexpressing HSP17.6A. The other sections in B are 5 independently obtained transgenic lines overexpressing c74.

Figure 12 shows the influence of *At-DBF2* expression in sense and antisense orientations on stress tolerance. BY2 cells were transformed by *A. tumefaciens* with recombinant T-DNA vectors containing At-DBF2 driven by CaMV 35S RNA promoter, pBIN-35S-At-DBF2 (upper left and right sections in A or diamonds in B), the CaMV 35S promoter and terminator pBIN-35S-CaMVter (bottom left sections in A or triangles in B), or antisense *At-DBF2* under the control of the CaMV 35S promoter pBIN-35S-ASAt-DBF2 (bottom right sections in A or circles in B). (A) Picture of the same amounts of transgenic cells after 3 weeks of growth on solid medium supplemented with 300 mM NaCl, 25% PEG, 2mM H_2O_2, or at 47°C (heat). (B) Growth of suspension cells in liquid medium. Upon stress, growth was measured as fresh weigth and expressed as a percentage of unstressed growth (control) (a). Stresses were applied after subculturing (= day 0) at indicated temperatures (e) and concentrations of NaCl (b) PEG (c), and H_2O_2 (f). For the cold shock (d), cells were maintained at 0°C for 2 days before the 2-week culture at 22°C. For each construction data of three

independent transgenic lines were pooled. To not overload the figure, SDs are not shown (maximum 15% of measured values). (C) Northern analysis of At-DBF2+TDBF2, kin1, and HSP17.6. Total RNAs were extracted from independent lines transformed with pBIN-35S-At-DBF2 (1) and (2), pBIN-35S-CaMter (3), and pBIN-35S-ASAt-DBF2 (4). Osmotic stress was induced with 10% PEG treatment for 5 hr (stressed).

Figure 13 shows the results of the growth of *A. thaliana* plants transformed with p35S-AtHSP17.6A and P35S control (upper right section) upon applying an osmotic stress induced by 20% PEG overnight. The results of two independent experiments are shown, each performed with 3 independently obtained transgenic lines overexpressing At-HSP17.6A (upper left and bottom left and right).

Figure 14 shows the results of the germination of *A. thaliana* plants transformed with p35S-Atc74 and P35S control (bottom section) on mineral medium supplemented with 125 mM NaCl. The results of two independent experiments are shown, each performed with 2 independently obtained transgenic lines overexpressing Atc74 (2 upper sections).

Table 1. Classification of the *Arabidopsis thaliana* clones isolated in Example 2. Clones isolated according to the description in example 2 have been analyzed on their potential to confer tolerance.According to the method described in example 2, the tolerance of different yeast transformants expressing an Arabidopsis cDNA to osmotic stress and salt stress was compared with the tolerance of DY wild type cells.

+	:	similar growth to the DY wild type cells;
++	:	growth of the transformant is visible at a 10-fold higher dilution (1:10) than control (1:1);
+++	:	growth of the transformant is visible at a 100-fold higher dilution (1:100) than control (1:1);
++++	:	growth of the transformant is visible at a 1000-fold higher dilution (1:1000) than control (1:1).

Table 2. Exemplary plant-expressible promoters for use in the performance of the present invention.

Table 3. Exemplary stress-inducible promoters for use in the performance of the present invention.

EXAMPLES

Example 1. Construction of the cDNA library.

Total RNA has been isolated from green siliques from *Arabidopsis thaliana* by grinding 1 g of siliques in 4 ml extraction buffer (100 mM tris-Hcl, pH 8, 10 mM EDTA, 100 mM LiCl) at 4° C, followed by phenolisation and chloroform: isoamylalcohol (24:1) extraction. To the aqueous phase, LiCl was added up to a final concentration of 2M, and the total RNA was allowed to precipitate overnight at 4°C. After centrifugation, the pellet was redissolved in 400 µl H_2O and reprecipitated with ethanol. Poly(A) messenger RNA was isolated from the total RNA by binding it to an oligo-dT cellulose spun column (Pharmacia), washing the column three times with 10 mM Tris-HCl, pH 7.5, 1 mM EDTA , 0.5 M NaCl and eluting the mRNA with 10 mM Tris-HCl, pH 7.5, 1 mM EDTA at 65° C.

The eluate was precipitated with ethanol, and cDNA was synthesized using MMLV- reverse transcriptase (Pharmacia) and a $d(T)_{14}$-XhoI primer for the first strand and *E. coli* DNA polymerase I (Pharmacia) for the second strand.

Example 2. Yeast transformation and selection for osmotolerance.

The cDNA was cloned into pYX vectors (Ingenius, R&D systems; 2 µ based pYX 212 for bank 1, ARS/CEN based pYX112 for bank 2) as EcoRI - XhoI fragments, using an Eco RI/Not I adaptor.

In these constructs, the cDNA is under the control of the strong constitutive TPI promoter. The yeast strain DY (MATa, *his3, can1-100, ade2, leu2, trp1, ura3*::3xSV40AP1-lacZ; kindly provided by N. Jones, Imperial Cancer Research Fund, London, UK) has been transformed with these cDNA libraries, using the Lithium Acetate transformation procedure (Gietz and Schietsl, 1995). After transformation with the Arabidopsis cDNA bank, transformants have been selected for the ability to grow in the presence of 100mM LiCl in a stepwise selection (Lee et al., 1999). LiCl is commonly used for salt tolerance screening in yeast (Haro et al. 1991). Several *A. thaliana* genes, conferring osmotolerance to the yeast, have been isolated (Table 1). To further analyse the potential of the selected Arabidopsis cDNA's to confer tolerance to environmental stress in yeast, each yeast transformant expressing such selected Arabidopsis cDNA's has been exposed to osmotic stress and salt stress. Each of the transformants was therefore grown for 16 hours in YPD (rich medium), and cell density was adjusted to OD_{600} at 2. Serial dilutions, 1:10, were made at three consecutive

steps. Ten microliters of each dilution was spotted on solid YPD medium (control) supplemented with 2 M sorbitol (osmotis stress) or 1.2 M NaCl (salt stress) and incubated at 28°C for 3 days. The results of this drop growth test (see also Lee et al., 1999) are shown in Table 1.

Example 3. Characterization of *At-DBF2.*

At-DBF2, a 1.8 kb cDNA (SEQ ID NO 1) has been identified in this screening that encodes a predicted 60.2 kDa protein showing 81 % similarity with the yeast Dbf2 transcriptional regulator. Homology (less than 40% similarity) has also be found with the putative Dbf2 homologues in human, C. elegans and Drosophila (named Ndr for nulear Dbf2 related, Millward *et al.* 1995). The *At-DBF2* deduced protein sequence (SEQ ID NO 2) contains the 11 domains of protein kinases (Figure 1A). Amino acids lying between the invariant residues D and N of domain VI do not match the features of serine/threonine specificity (LKPE) defined by Hanks *et al.* (1988) but the GSPDYIALE peptide in domain VIII does well indicate serine/threonine specificity and *At-DBF2* can complement the yeast *dbf2* mutant (Figure 1B).

In mature Arabidopsis plants, *At-DBF2* is expressed in all tested organs. The highest abundance of transcripts has been found in siliques. A Southern analysis in Arabidopsis, tobacco and tomato has revealed that *DBF2* seems to be conserved in plants (see Example 13 below). As *At-DBF2* has been identified in a screening for LiCl tolerance, its effect in other stress situations has been tested in yeast (Figure 2).

Example 4. Overexpression of *Arabidopsis* and *Saccharomyces cerevisiae DBF2* enhances cold, heat, salt and drought tolerance in yeast.

In order to test whether the effect was specific to the plant gene, the yeast *DBF2* gene has been overexpressed in the same vector. Upon a drop growth test (Figure 2 and Lee et al., 1999). A remarkable enhancement of stress tolerance can be seen at 42°C, during osmotic stress (sorbitol), and after salt and cold treatments in yeast. There is no difference between stress tolerance afforded by the plant or the yeast gene. The enhancement of stress tolerance due to the overexpression of *At-DBF2* or *DBF2* reflects a role for these genes in stress situations. Therefore yeast and Arabidopsis plants have been exposed to sorbitol- and PEG-induced osmotic stress. *At-DBF2* as well as *DBF2* is induced rapidly (1 to 2 hours) and transiently upon osmotic stress (Figure 3A). The expression of *At-DBF2* and *DBF2* has been analyzed during other environmental stresses in Arabidopsis plants or in yeast cells after the

time corresponding to the highest induction seen in Fig. 3A (Figure 3B). In plant as in yeast, there is a clear induction after heat, salt, osmotic and to a lesser extent after cold, which perfectly correlates with stresses to which the overexpression enhances tolerance. However, many genes are induced upon stress without relevant adaptive role, amongst others because post-transcriptional mechanisms inhibit subsequent translation. Here *At-DBF2* protein amount, as detected by anti-Dbf2 antibodies, clearly increased upon stress (Figure 3C).

Example 5. Both *At-DBF2* and *DBF2* can functionally complement the *hog1* mutation.

To investigate a possible interaction between stress signaling pathways and *DBF2*, the salt sensitive hog1 mutant was transformed with *At-BDF2* and *DBF2*. The *HOG1* MAP kinase pathway regulates osmotic induction of transcription in yeast (Schuller *et al.* 1994). The osmosensitivity of the mutant could be recovered by the overexpression of both *DBF2* and *At-DBF2* (Figure 4).

Example 6. *At-DBF2* is cell cycle regulated.

DBF2 expression is cell cycle regulated where it plays a role in DNA synthesis initiation but also in nuclear division through its association with the CCR4 complex (Komarnitsky *et al.* 1998, Johnston *et al.* 1990). This regulation was investigated in plants. A tobacco BY-2 cell line in which the highest level of culture synchronization, compared with other plant cell lines has been achieved so far (Shaul *et al.* 1996, Reicheld *et al.* 1995) was used. Stationary phase cells were diluted into fresh medium and treated with aphidicolin (blocking cells in the beginning of the S phase) for 24 hours, then washed. The percentage of synchronous mitosis after release from the aphidicolin block was about 65 % (Figure 5A-B). A 1.6-Kb tobacco *DBF2* homologue (*T-DBF2*) could be detected on Northern blot with the *At-DBF2* as a probe. *T-DBF2* steady-state transcript level clearly oscillates during the cell cycle and is mainly present during S, decreases during G2 until late M from where it increases until a peak in S phase. *T-DBF2* expression occurs clearly before *CYCB1.2* (a marker of G2-M phases), but parallels the one of H4 (a S phase marker) except at the S/G2 transition, where *T-DBF2* transcripts decline earlier, and at the M/G1 transition, where *T-DBF2* expression increases earlier. The use of the cell cycle markers CYCB1.2 and H4 is described in Reicheld et al.

To follow unperturbed G1 and S phases, BY2 cell suspension was synchronized using a double blocking procedure (Nagata *et al.*,1992). After the release from the aphidicoline block, cells are treated for 4 hours with propyzamide in the beginning of the preprophase. The percentage of synchronous mitosis after the release from the propyzamide block was higher than 75%. *T-DBF2* was periodically expressed with an undetectable expression until late M, a sharp increase in G1 and a peak in mid S (Figure 5C-D) which confirms results of Figures 5A-B. However a function for the plant *DBF2* in cell cycle can only be assigned with measurement of the kinase activity. In yeast, *DBF2* transcript levels do not correlate with kinase activation which occurs by dephosphorylation (Toyn and Johnson, 1994). The precise function of Dbf2 in regulation of the cell cycle is not known. An essential role has been proposed during anaphase or telophase. No activity has been measured in G1 despite evidence for a role for Dbf2 in initiation of DNA synthesis.

As other proteins recently identified, Dbf2 controls the M/G1 transition which is a major cell cycle transition in yeast (Aerne *et al.* 1998). The existence of a M/G1 control checkpoint has been suggested in plant cells (Hemmerlin and Bach 1998) but its importance compared to G1/S and G2/M has not been investigated.

Overexpression of *DBF2* in yeast results in kinase activity throughout the cell cycle, which may be due to the saturation of a post-translational deactivating mechanism (Toyn and Johnston, 1994). Overexpression of the functionnally conserved *At-DBF2* has most probably the same effect. However, the presence of Dbf2 kinase activity at the wrong time in the cell cycle does apparently not affect its progression. In marked contrast constitutive activity has a marked effect on stress tolerance. The role played by *At-DBF2* or *DBF2* in stress is most probably independent from the cell division cycle. *At-DBF2* expression is present in all plant organs (abundant expression is observed in stems where only 1-2 % cells have a mitotic activity) and can be rapidly induced upon stress. However, a link with the cell cycle is not excluded. Higher stress tolerance in yeast overexpressing *DBF2* or *At-DBF2* may be correlated to the overproduction of the kinase in G1 where yeast cells are particularly sensitive to stress. Most plant cells are also thought to be blocked in G1 but the relationship with stress response is poorly known.

Example 7. Tobacco cell transformation and recombinant T-DNA Vector construction

BY2 cells were stably transformed as described (Shaul et al., 1996) by *Agrobacterium tumefaciens* C58C1Rif^R (pGV2260) strain (Deblaere et al., 1985) carrying pBIN-35S-At-DBF2 or pBIN-35S-ASAt-DBF2 recombinant binary vectors. PBIN-35S-At-DBF2 is the plant binary vector pBIN m-gfp4 in which the BamHI-SacI fragment containing the gfp reporter gene was replaced with a BamHI-SacI fragment containing the At-DBF2 cDNA from pYX-At-DBF2. p-Bin-35S-CaMVter is the plant binary vector pBIN19 in the HindIII-SacI restriction sites of which the hindIII-SacI fragment of pDH51 containing the cauliflower mosaic virus (CaMV) 35S RNA promoter and terminator was cloned. pBIN-35S-ASAt-DBF2 is the pBIN-35S-CaMVter vector in which the At-DBF2 cDNA was cloned in the antisense orientation from pYXAt-DBF2 in the BamHI-SmaI restriction sites, between the CaMV 35S RNA promoter and terminator. More details are described in Lee et al. (1999).

Example 8. Overexpression of At-DBF2 sense and antisense RNA in plant cells

Transgenic plant cells overexpressing *At-DBF2* were generated to test the role of this protein in stress tolerance *in planta*. Tobacco BY2 cells were stably transformed by *A. tumefaciens* carrying the *At-DBF2* cDNA driven by the strong constitutive CaMV 35S RNA promoter. The antisense *At-DBF2* RNA also was overexpressed under the control of the same promoter. Control lines were obtained by transforming tobacco BY2 cells with pBIN-35S-CaMVter. Three independently obtained *At-DBF2*-overexpressing tobacco transgenic cell lines have been selected with a high and similar *At-DBF2* expression and analysed further. Three tobacco transgenic cell lines overexpressing antisense *At-DBF2* were chosen that showed an undetectable tobacco DBF2 transcript level. Both the overexpression of *At-DBF2* and the down-regulation of the endogenous gene by the antisense strategy did not result in significant differences in growth after 2 weeks (Fig. 12A and 12B). On the contrary, marked differences in growth were observed after a 2-week treatment with NaCl, PEG-induced drought, cold, or high temperatures. Transgenic lines that overexpressed *At-DBF2* were clearly more tolerant than control lines. Inhibition of the endogenous DBF2 expression was correlated with a higher sensitivity to those stresses. To understand the basis of stress

tolerance in *At-DBF2*-overexpressing plant cells, expression of stress-induced genes was followed in control and stress conditions (Fig. 12C). Tobacco kin1 and HSP17.6A homologues already were induced in *At-DBF2*-overexpressing tobacco cells in control conditions to a level similar to that observed during stress conditions (PEG-induced drought), suggesting that *At-DBF2* overexpression may mimic a stress signal.

Example 9. Arabidopsis transformation and recombinant T-DNA vector construction with genes conferring tolerance to environmental stress

Arabidopsis were stably transformed as described in Clarke, Wei and Lindsey (1992) by Agrobacterium tumefaciens C58C1RifR (pGV2260) strains carrying pBIN-35S-At-DBF2, pBIN-35S-At-HSP17.6A, pBIN-35S-At-c74 recombinant binary vectors. pBIN-35S-At-DBF2 is described in Lee et al. 1999. pBIN-35S-At-HSP17.6A recombinant binary vector was constructed as following: the EcoRI-XhoI fragment containing At-HSP17.6A cDNA in pYX-HSP17.6A (recombinant pYX212) was first cloned in pYES2 (Invitrogen) resulting in pYES-HSP17.6A. Than the BamHI-SphI fragment of pYES-HSP17.6A containing the At-HSP17.6A cDNA was cloned in the plant binary vector pBIN m-gfp4 in which the BamHI-SacI fragment containing the gfp receptor gene was deleted and replaced by the At-HSP17.6A cDNA. The 3' protruding ends generated by SacI and SphI were blunt ended by T4 DNA polymerase. pBIN-35S-c74 was constructed with a similar strategy as pBIN-35S-AtHSP17.6A with an intermediary pYES-Atc74 vector. The At-c74 cDNA was first amplified with PCR using the primers 5' AAA AAA CAC ATA CAG GAA TTC 3' (SEQ ID NO 122) and 5' AGT TAG CTA GCT GAG CTC GAG 3' (SEQ ID NO 123), then cloned "blunt ended" in the vector pYES2 cut with NotI and BstXI and blunt ended with T4 DNA polymerase. Subsequently, the BamHI-SphI fragment of pYES-c74 was cloned in pBINm-gfp4 as explained supra.

Example 10. Tolerance to environmental stress in plant cells

Transgenic calli were isolated from each of the transgenic Arabidopsis lines transformed with At-DBF2, At-HSP17.6A and At-c74. The growth of these transgenic calli during salt stress was measured and compared with control calli derived from transgenic Arabidopsis lines transformed with pBIN-35S-CaMVter. Callus pieces (25 for each transgenic line) of similar fresh weight (50 to 100 mg) were therefor grown on callus inducing medium (Clarke et al., 1992) supplemented with 200mM NaCl. After two weeks, from visual inspection, it was clear that transgenic calli transformed with

At-DBF2 or At-HSP17.6A or At-c74 looked much better than control transgenic calli transformed with pBIN-35S-CaMVter. The latter calli turned yellow and started dying. To confirm the observation, the fresh weight of the calli was measured. In comparison with the control transgenic calli, the fresh weight of the transgenic calli was for each of the three lines at least five times higher than the fresh weight of the control trangenic calli.

Example 11. Tolerance to environmental stress in plants.

Seeds from transgenic Arabidopsis plants tranformed with pBIN-35S-At-DBF2, p-BIN-35S-At-c74, or pBIN-35S-At-HSP17.6A, were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-AS+At-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark, 70 microeinsteins. After 9 days growth, filters were transferred to liquid K1 medium supplemented with 200 mM NaCl for overnight incubation. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium. Under these conditions, the control transgenic plants turned yellow, their growth was inhibited and eventually they died. On the contrary, the transgenic lines transformed with At-DBF2 or At-HSP17.6A or At-c74 survived very well (Figure 6 and Figure 11).

To further evaluate the scope of protection to environmental stress, transgenic plants were exposed to osmotic stress. Therefor seeds from transgenic Arabidopsis plants transformed with pBIN-35S-At-DBF2, pBIN-35S-At-c74 or pBIN-35S-At-HSP17.6A were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-ASAt-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark,

70 microeinsteins. After 9 days growth, filters were transferred to liquid K1 medium supplemented with 20 % polyethylene glycol for overnight incubation. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium. Under these conditions, the control transgenic plants turned yellow, their growth was inhibited and eventually they died. On the contrary, the transgenic lines transformed with At-DBF2, At-HSP17.6A or At-c74 survived very well (see Figure 7 and 13). Their growth was comparable to growth on control medium without polyethylene glycol.

To further analyse the scope of protection to environmental stress, transgenic plants were exposed to high and low temperatures. Therefor seeds from transgenic plants transformed with pBIN-35S-At-DBF2 or pBIN-35S-At-c74 were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-ASAt-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark, 70 microeinsteins. After 9 days growth, for the experiments with high temperature stress, plants were exposed to 48°C for two hours. For the experiments with low temperature stress, plants were exposed to gradually decreasing temperatures, down to -7°C. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium.

Under both low temperature and high temperature stress, the growth of control transgenic plants was inhibited and eventually they died. The transgenic lines transformed with At-DBF2 or At-c74 survived very well. Their growth was comparable to growth under control conditions with normal temperature (see Figure 8 and 9).

To further analyse the scope of protection to environmental stress, transgenic plants were exposed to salt stress during germination. Sterilized mature seeds from transgenic plants transformed with pBIN-35S-At-DBF2 or pBIN-35S-At-c74 were placed on top of petri dishes containing MS (Murashige and Skoog) medium with 0,8 % agar and 30 g l^{-1} sucrose. Control plants were the ones transformed with pBIN-35S-CaMVter. Prior to germination and pH 5.7 adjustment, NaCl was added to a final concentration of 125 mM. Three petri dishes with a mean of 40-50 seeds per dish were used per treatment in every experiment. The complete experiment was repeated

twice. Seed germination at 22°C was followed. Seeds were considered to germinate after radical and green cotyledon emergency occurred.

On control medium (without 125 mM NaCl), germination of all transgenic lines was very similar to each other and to wild type plants. On medium supplemented with 125 mM NaCl, seeds from transgenic lines overexpressing At-DBF2 or At-c74 germinate significantly better than control transgenic lines. Less than 10 % of the seeds from transgenic lines transformed with pBIN-35S-CaMVter germinate under these conditions. In contrast, more than 70 % of the seeds from trangenic lines overexpressing At-DBF2 or At-c74 germinate on medium containing 125 mM NaCl (Figure 14).

Example 12. Southern hybridisation of At-DBF2 genes in other plants

To investigate whether *DBF2* homologues exist in other plant species, a Southern hybridisation analysis was performed using the full length *At-DBF2* as a probe. Genomic DNA was extracted from tobacco, tomato and rice according to Dellaporta et al. (1983) and further purified by phenol :chloroform extractions.

DNA (10 µg) was digested with restriction enzymes and separated on 1% (w/v) agarose gels using Lambda DNA digested with Hind III as molecular size standards. The DNA was transformed on to nylon membranes (Hybond N ; Amersham, little Chalfont, UK) in 0.4 N NaOH. Filters were UV-cross-linked for 30 seconds, prehybridized for 3 hours at 56°C in hybridization solution (2x SSPE, 0.1%(w/v) SDS, 5x Denhardt solution) using 200 gm^{-3} denatured salmon sperm DNA, and hybridized overnight with radiolabelled probes. 1X SSPE was 0.15 M NaCl/ 0.01 M sodium dihydrogen phosphate/ 1 mM EDTA .

Filters were washed at 56°C in 2x SSPE, 0.1% (w/v) SDS for 20 min, then 1x SSPE, 0.1% (w/v) SDS for 20 min, and finally in 0.1x SSPE, 0.1% (w/v) SDS for 20 min. Filters were exposed to X-ray film (Kodak X-AR ; Kodak, NY, USA) in the presence of intensifying screens for 24 hours.

The results of the hybridisation experiments show that tobacco, tomato and rice have at least one homologue to At-DBF2.

<u>Tabel 1</u>

putative function in	Features of encoded protein	SEQ ID NO.	Growth on medium with1,2 M NaCl	growth on medium with 2,0 M sorbitol
signalling	Similar to a yeast DBF2 cell cycle protein	1	++++	++++
metabolism	HSP17.6A	3	++++	++++
unknown	C74	5	+++	+++
metabolism	Similar to ADH2	7	+	++++
metabolism	Similar to D. melanogaster catalase/catalase 3	9	++++	+
metabolism	Similar to the HSP90 heat shock protein family	11	++++	++++
metabolism	similar to phosphoenolpyruvate carboxylase	13	+	+++
metabolism	pathogen related proteins, class 10	15	+	++++
metabolism	Arabidopsis ascorbate peroxidase	17	++++	++++
metabolism	similar to phosphatase binding protein	19	++++	++++
metabolism	similar to phosphatase binding protein	21	++++	++++
metabolism	similar to retinol dehydrogenase	23	+++	++++
metabolism	similar to retinol dehydrogenase	25	++++	++++
metabolism	ribosomal protein	27	++++	++++
metabolism	ribosomal protein	29	++++	++++
metabolism	similar to a protein transporter (kinase homolog)	31	++++	++++
metabolism	similar to a peptide transporter	33	++++	+
metabolism	similar to a wheat low affinity cation transporter LCT1	35	++++	++++
metabolism	similar to yeast iso-1-cytochrome c (CYC-1)	37	++++	++++
metabolism	similar to yeast OSM1	39	++++	++++
metabolism	similar to yeast copper uptake gene (CUP1)	41	++++	+++
metabolism	similar to yeast UV-induced damage repair protein (RAD7)	43	++++	++++
metabolism	electron transporter, apocytochrome b	45	++++	++++
metabolism	similar to membrane lipoprotein LPPL1	47	++++	++++
metabolism	similar to tobacco auxin binding protein	49	+	++++
metabolism	similar to tobacco cytokinin binding protein CBP 57	51	+++	++++
signalling	similar to calcium binding protein yeast calcineurin B	53	+++	++++

signalling	similar to calcium binding protein glycine max calnexin	55	++++	+++
signalling	similar to calcium binding protein Dictyostelium discoideum calreticulin	57	++++	++++
signalling	similar to calcium binding protein calmodulin 1	59	++++	+
signalling	similar to calcium binding protein calmodulin 2	61	+	++++
signalling	MAP kinase kinase, homologous to Dyctyostelium mekA (DdMek1)	63	++++	+++
signalling	similar to human adenosine kinase	65	+	++++
signalling	similar to human tyrosine kinase	67	++++	++++
signalling	similar to common ice plant tyrosine kinase	69	++++	++++
signalling	similar to the yeast protein kinase C receptor	71	++++	++++
signalling	similar to tobacco and Arabidopsis HAT7 homeotic protein	73	++	++++
signalling	similar to E. coli sigma factor regulator (RSEB)	75	+	++++
signalling	similar to human protein phosphatase 2C	77	++++	++++
metabolism	late embryogenesis abundant proteins, Arabidopsis LEA protein 10 & 14	79	++	++++
metabolism	late embryogenesis abundant proteins, Arabidopsis LEA protein 10 & 14	81	++	++++
metabolism	pathogen related proteins, class 10	83	++++	++++
metabolism	cell wall peroxidase	85	++++	+++
metabolism	ribosomal protein	87	+++	++++
metabolism	salt stress induced protein, SAS 1	89	++++	++++
metabolism	PR gene (AIG2)	91	++++	++++
metabolism	MT1c	93	++++	++++
metabolism	IPP2 (Isopentenyl diphosphate)	95	+++	++++
metabolism	chlorophyll a/b binding protein	97	+++	+++
metabolism	glutathione transferase	99	++	++++
signalling	cold- and ABA inducible, calcium dependent – kinase, Kin1	101	++++	++++
signalling	MAP kinase, Atmpk1	103	++	++++
signalling	Arabidopsis cell cycle protein histone H2A	105	++++	++++
unknown	chromosome 4 – sequence	107	+++	++++
unknown	chromosome 4 – sequence	109	+	++++
unknown	chromosome 5 – sequence	111	++++	+++
unknown	chromosome 5 – sequence	113	++++	++
unknown	chromosome 5 – sequence	115	++++	++++
unknown	chromosome 5 – sequence	117	+	++++
unknown	chromosome 5 – sequence	119	+	++++

signalling	similar to calcium binding protein centrin (caltractin)	121	++++	++++

TABLE 2
EXEMPLARY PLANT-EXPRESSIBLE PROMOTERS FOR USE IN THE PERFORMANCE OF THE PRESENT INVENTION

GENE SOURCE	EXPRESSION PATTERN	REFERENCE
α-amylase (*Amy32b*)	Aleurone	Lanahan *et al* (1992); Skriver *et al.* (1991)
cathepsin β-like gene	Aleurone	Cejudo *et al.* (1992)
Agrobacterium rhizogenes rolB	Cambium	Nilsson *et al.* (1997)
PRP genes	cell wall	http://salus.medium.edu/mmg/tierney/html
barley *ltr1* promoter	Endosperm	
synthetic promoter	Endosperm	Vicente-Carbajosa *et al.*(1998)
AtPRP4	Flowers	http://salus.medium.edu/mmg/tierney/html
chalene synthase (chsA)	Flowers	van der Meer *et al.* (1990)
apetala-3	Flowers	
Chitinase	fruit (berries, grapes, etc)	Thomas *et al.* CSIRO Plant Industry, Urrbrae, South Australia, Australia; http://winetitles.com.au/gwrdc/csh95-1.html
rbcs-3A	green tissue (eg leaf)	Lam *et al.* (1990); Tucker *et al.* (1992)
leaf-specific genes	Leaf	Baszczynski *et al.* (1988)
AtPRP4	Leaf	http://salus.medium.edu/mmg/tierney/html
Pinus cab-6	Leaf	Yamamoto *et al.* (1994)
SAM22	Senescent leaf	Crowell *et al.* (1992)
R. japonicum nif gene	Nodule	United States Patent No. 4, 803, 165
B. japonicum nifH gene	Nodule	United States Patent No. 5, 008, 194

GmENOD40	Nodule	Yang *et al.* (1993)
PEP carboxylase (PEPC)	Nodule	Pathirana *et al.* (1992)
Leghaemoglobin (Lb)	Nodule	Gordon *et al.* (1993)
Tungro bacilliform virus gene	Phloem	Bhattacharyya-Pakrasi *et al.* (1992)
sucrose-binding protein gene	plasma membrane	Grimes *et al.* (1992)
pollen-specific genes	pollen; microspore	Albani *et al.* (1990); Albani *et al.* (1991)
maize pollen-specific gene	Pollen	Hamilton *et al.* (1992)
sunflower pollen-expressed gene	Pollen	Baltz *et al.* (1992)
B. napus pollen-specific gene	pollen;anther; tapetum	Arnoldo *et al.* (1992)
root-expressible genes	Roots	Tingey *et al.* (1987); An *et al.* (1988);
tobacco auxin-inducible gene	root tip	Van der Zaal *et al.* (1991)
β-tubulin	Root	Oppenheimer *et al.* (1988)
Tobacco root-specific genes	Root	Conkling *et al.* (1990)
B. napus G1-3b gene	Root	United States Patent No. 5, 401, 836
SbPRP1	Roots	Suzuki *et al.* (1993)
AtPRP1; AtPRP3	roots; root hairs	http://salus.medium.edu/mmg/tierney/html
RD2 gene	root cortex	http://www2.cnsu.edu/ncsu/research
TobRB7 gene	root vasculature	http://www2.cnsu.edu/ncsu/research
AtPRP4	leaves; flowers; lateral root primordia	http://salus.medium.edu/mmg/tierney/html
Seed-specific genes	Seed	Simon *et al.* (1985); Scofield *et al.* (1987); Baszczynski *et al.* (1990)
Brazil Nut albumin	seed	Pearson *et al.* (1992)
Legumin	Seed	Ellis *et al.* (1988)
Glutelin (rice)	Seed	Takaiwa *et al.* (1986);Takaiwa *et al.*

		(1987)
Zein	Seed	Matzke *et al.* (1990)
NapA	Seed	Stalberg *et al.* (1996)
Sunflower oleosin	seed(embryo and dry seed)	Cummins *et al.* (1992)
LEAFY	shoot meristem	Weigel *et al.* (1992)
Arabidopsis thaliana knat1	shoot meristem	Accession number AJ131822
Malus domestica kn1	shoot meristem	Accession number Z71981
CLAVATA1	shoot meristem	Accession number AF049870
Stigma-specific genes	Stigma	Nasrallah *et al.* (1988); Trick *et al.* (1990)
Class I patatin gene	Tuber	Liu *et al.* (1991)
Blz2	Endosperm	EP99106056.7
PCNA rice	Meristem	Kosugi *et al* (1991); Kosugi and Ohashi (1997)

Table 3. Stress inducible promoters

Name	Stress	Reference
P5CS (delta(1)-pyrroline-5-carboxylate syntase)	salt, water	Zhang et al; Plant Science. Oct 28 1997; 129(1): 81-89
cor15a	Cold	Hajela et al., Plant Physiol. 93: 1246-1252 (1990)
cor15b	Cold	Wlihelm et al., Plant Mol Biol. 1993 Dec; 23(5):1073-7
cor15a (-305 to +78 nt)	cold, drought	Baker et al., Plant Mol Biol. 1994 Mar; 24(5): 701-13
rd29	salt, drought, cold	Kasuga et al., Nature Biotechnology, vol 18, 287-291, 1999
heat shock proteins, including artificial promoters containing the heat shock element (HSE)	Heat	Barros et al., Plant Mol Biol, 19(4): 665-75, 1992. Marrs et al., Dev Genet.,14(1): 27-41, 1993. Schoffl et al., Mol Gen Gent, 217(2-3): 246-53, 1989.
smHSP (small heat shock proteins)	heat	Waters et al, J Experimental Botany, vol 47, 296, 325-338, 1996
wcs120	Cold	Ouellet et al., FEBS Lett. 423, 324-328 (1998)
ci7	Cold	Kirch et al., Plant Mol Biol, 33(5): 897-909, 1997 Mar
Adh	cold, drought, hypoxia	Dolferus et al., Plant Physiol, 105(4): 1075-87, 1994 Aug
pwsi18	water: salt and drought	Joshee et al., Plant Cell Physiol, 39(1): 64-72, 1998, Jan
ci21A	Cold	Schneider et al., Plant Physiol, 113(2): 335-45, 1997
Trg-31	Drought	Chaudhary et al., Plant Mol Biol, 30(6): 1247-57, 1996
Osmotin	Osmotic	Raghothama et al., Plant Mol Biol, 23(6): 1117-28, 1993

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Claims

1. A method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.

2. An isolated polynucleic acid obtainable by a method according to claim 1.

3. The isolated polynucleic acid of claim 2 which encodes a polypeptide as listed in Table 1.

4. The isolated polynucleic acid of claim 3, which is chosen from:
   (a) any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121, or the complementary strands thereof;
   (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
   (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
   (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

5. The isolated polynucleic acid of any of claim 2 to 4, which encodes a plant homolog of yeast DBF2 kinase.

6. The isolated polynucleic acid of claim 5, which is chosen from:
   (a) SEQ ID NO 1, or the complementary strands thereof;
   (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;

(c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
(d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

7. Use of an isolated polynucleic acid of claims 2 to 3 which encodes an HSP 17.6A protein for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

8. Use of an isolated polynucleic acid of claim 7 for expression of the protein encoded thereby in a plant cell, with said polynucleic acid being chosen from:
(a) SEQ ID NO 3, or the complementary strand thereof;
(b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
(c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
(d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

9. Use of an isolated polynucleic acid as defined above which is chosen from:
(a) any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or the complementary strand thereof;
(b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
(c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
(d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

10. The isolated polynucleic acid of any of claims 2 to 4, which encodes a c74 protein which is chosen from:
    (a) SEQ ID NO 5, or the complementary strand thereof;
    (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
    (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
    (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

11. An isolated polypeptide encoded by a polynucleic acid according to or as defined in any of claims 2 to 10, or a functional fragment thereof.

12. The isolated polypeptide of claim 11 having at least part of the sequence of any of SEQ ID NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120.

13. A method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising transiently introducing into a plant cell a recombinant DNA comprising a polynucleic acid of or as defined in any of claims 2 to 10 which is expressed in an amount effective to confer enhanced tolerance or resistance to environmental stress.

14. A method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising stably introducing into a plant cell a recombinant DNA comprising a polynucleic acid of or as defined in any of claims 2 to 10 which is expressed in an amount effective to confer enhanced tolerance or resistance to environmental stress.

15. The method of claims 13 or 14 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claims 5 or 6 encoding a plant DBF2 kinase.

16. The method of claim 16 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claims 7 or 8 encoding an HSP 17.6A protein.

17. The method of claim 13 to 14 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claim 10 encoding a c74 protein.

18. The method of any of claims 13 to 17, comprising introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:
   - a polynucleic acid according to or as defined in any of claims 2 to 10, and,
   - a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control of said plant-expressible promoter.

19. A method for producing a plant with enhanced tolerance or resistance to environmental stress, comprising introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:
   - a DNA encoding a protein which when expressed in said plant cell at an effective amount indirectly increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or indirectly increases or induces the activity of a polypeptide of claims 11 or 12, and,

- a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.

20. A method of claim 19 wherein said DNA encodes a sense or antisense RNA molecule or a ribozyme capable of increasing or inducing the expression of said endogenous polynucleic acid sequence according to or as defined in any of claims 2 to 10.

21. A recombinant polynucleic acid comprising:
a polynucleic acid according to or as defined in any of claims 2 to 10, and,
a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control of said plant-expressible promoter.

22. A recombinant polynucleic acid comprising:
(a) a DNA encoding a protein which when expressed in said plant cell at an effective amount increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or increases or induces the activity of a polypeptide of claims 11 or 12, and,
(b) a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.

23. The recombinant polynucleic acid of claim 22, wherein said DNA encodes an anti-sense RNA, a ribozyme or a sense RNA which when expressed in a cell of a plant increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or which induces or increases the activity of a protein of claim 11 or 12.

24. The recombinant polynucleic acid of claim 21 comprising at least part of the nucleotide sequence of any of SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, or part thereof.

25. The recombinant polynucleic acid of claim 21 to 24 comprising at least part of the coding sequence of a gene encoding a protein as listed in Table 1.

26. The recombinant polynucleic acid of any of claims 21 to 25 wherein said plant-expressible promoter is a constitutive promoter.

27. The recombinant polynucleic acid of any of claims 21 to 25 wherein said plant-expressible promoter is a stress-inducible or organ- or tissue-specific promoter.

28. The recombinant polynucleic acid of any of claims 21 to 26 wherein said plant-expressible promoter is the 35S promoter of CaMV.

29. A recombinant host cell transformed with at least one isolated polynucleic acid of or as defined in any of claims 2 to 10.

30. A plant cell transformed with a recombinant polynucleic acid of any one of claims 21 to 28.

31. A plant consisting essentially of plant cells of claim 30.

32. A callus consisting essentially of plant cells of claim 30.

33. A harvestable part, organ, tissue or propagation material of a plant of claim 31, comprising said recombinant DNA.

34. The use of a recombinant polynucleic acid of claim 21 to 28 to produce transgenic plants.

35. A probe which is part of the polynucleic acid sequence of or as defined in any of claims 2 to 10 and which hybridizes specifically with said polynucleic acid or the complement thereof.

36. A primer which is part of the polynucleic acid sequence of or as defined in any of claims 2 to 10 and which specifically amplifies said polynucleic acid or the complement thereof.

37. A composition comprising a polynucleic acid sequence of or as defined in any of claims 2 to 10, a polypeptide of claim 11 or 12, a probe of claim 35 or a primer of claim 36.

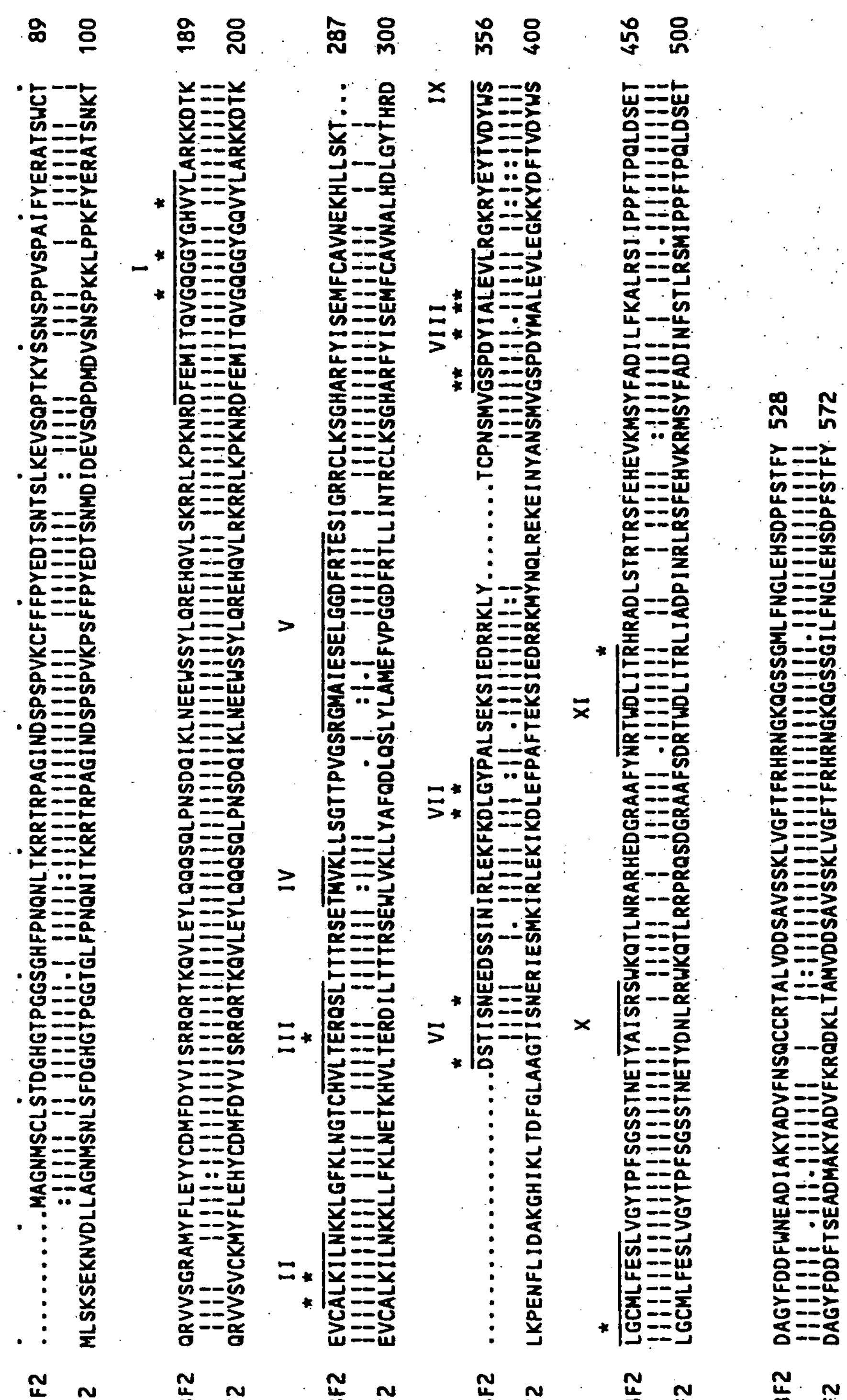


FIGURE 1 A

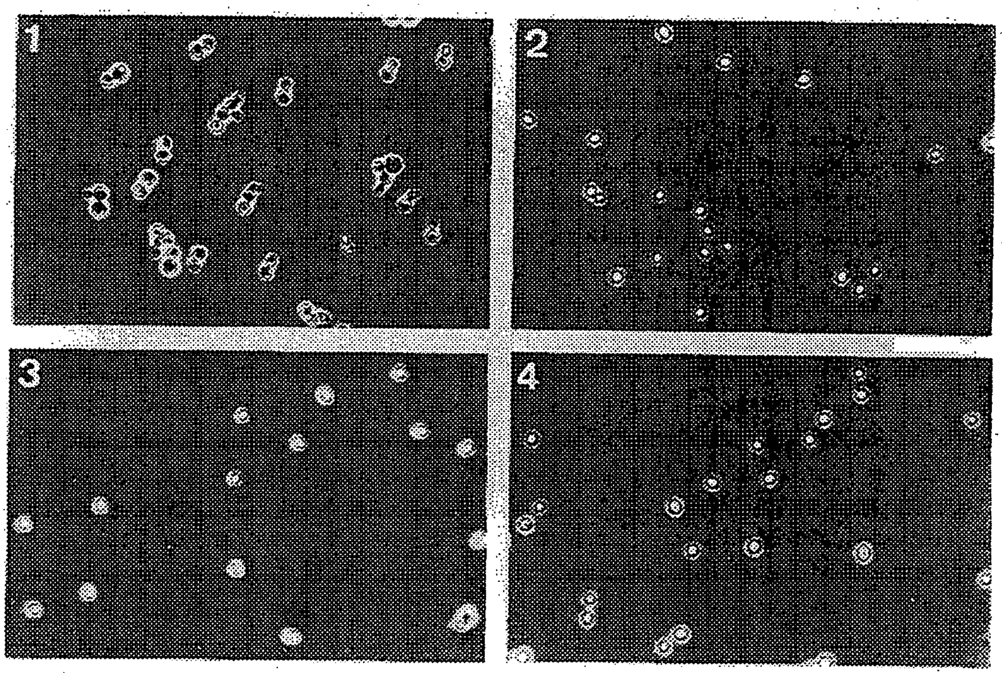
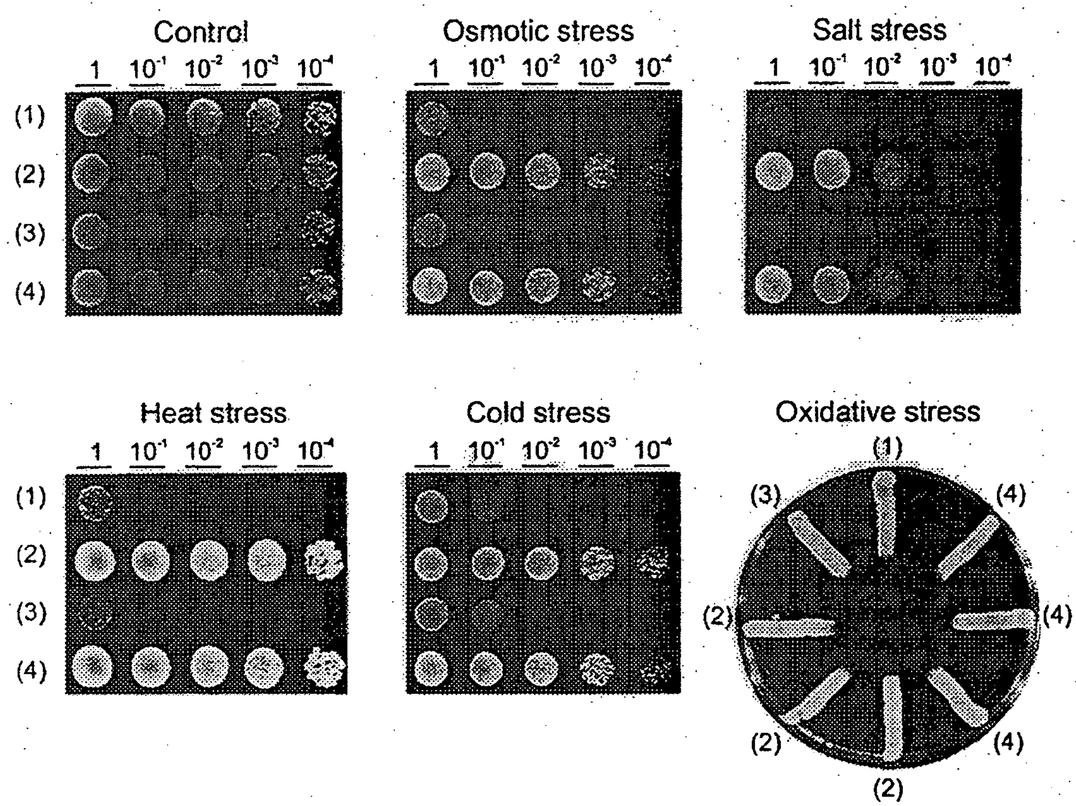


FIGURE 1B


Control
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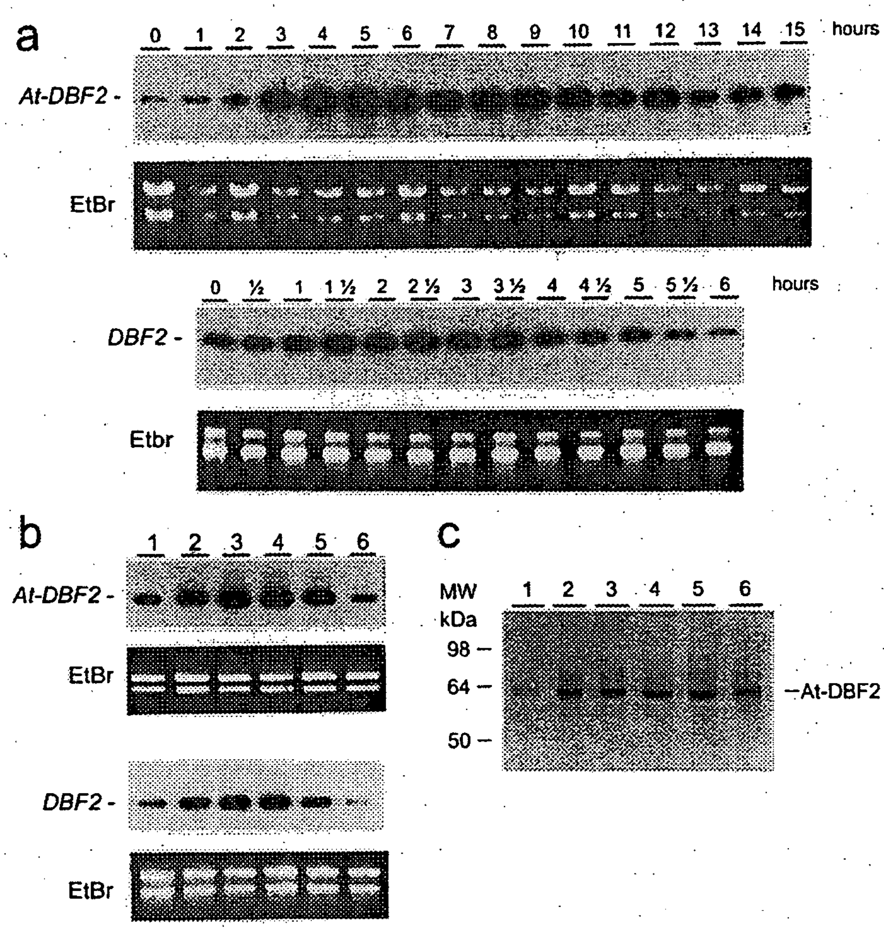
10^{-2}
10^{-3}
10^{-4}
(1)
(2)
(3)
(4)
Osmotic stress
Salt stress
Heat stress
Cold stress
Oxidative stress

FIGURE 2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0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 hours
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EtBr
0 ½ 1 1 ½ 2 2 ½ 3 3 ½ 4 4 ½ 5 5 ½ 6 hours
DBF2 -
Etbr
b
1 2 3 4 5 6
At-DBF2 -
EtBr
DBF2 -
EtBr
c
MW
kDa
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98 —
64 —
50 —
—At-DBF2

FIGURE 3

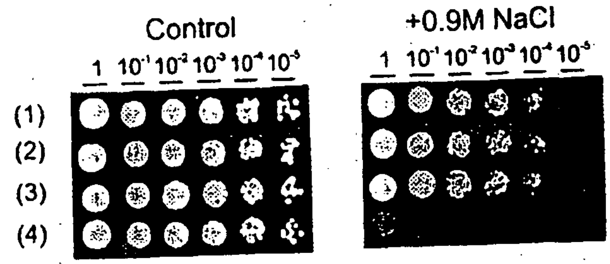


FIGURE 4

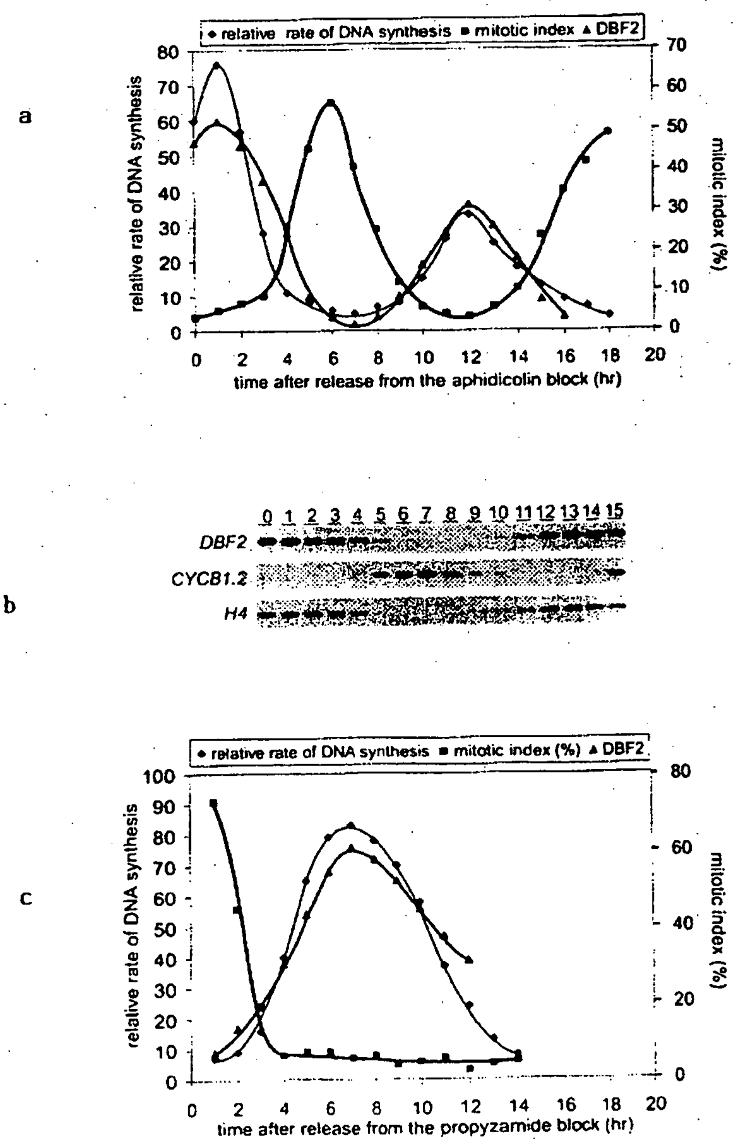


FIGURE 5

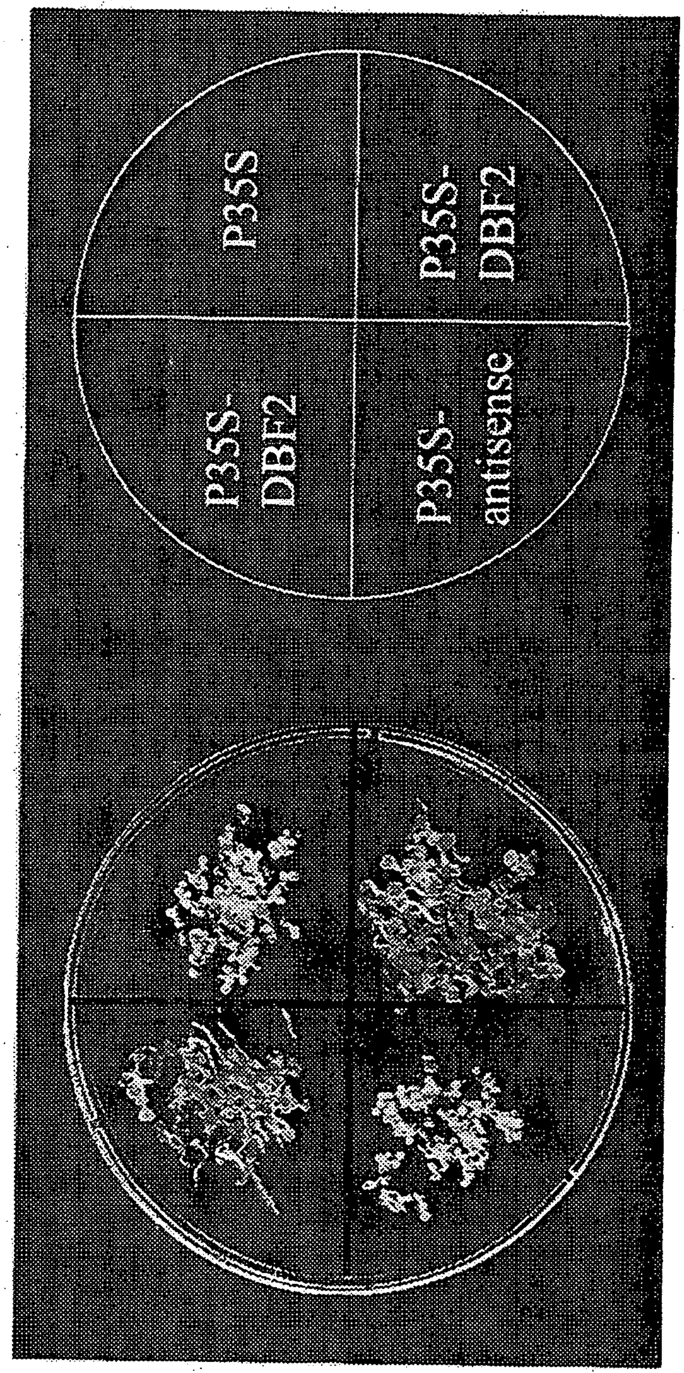


FIGURE 6

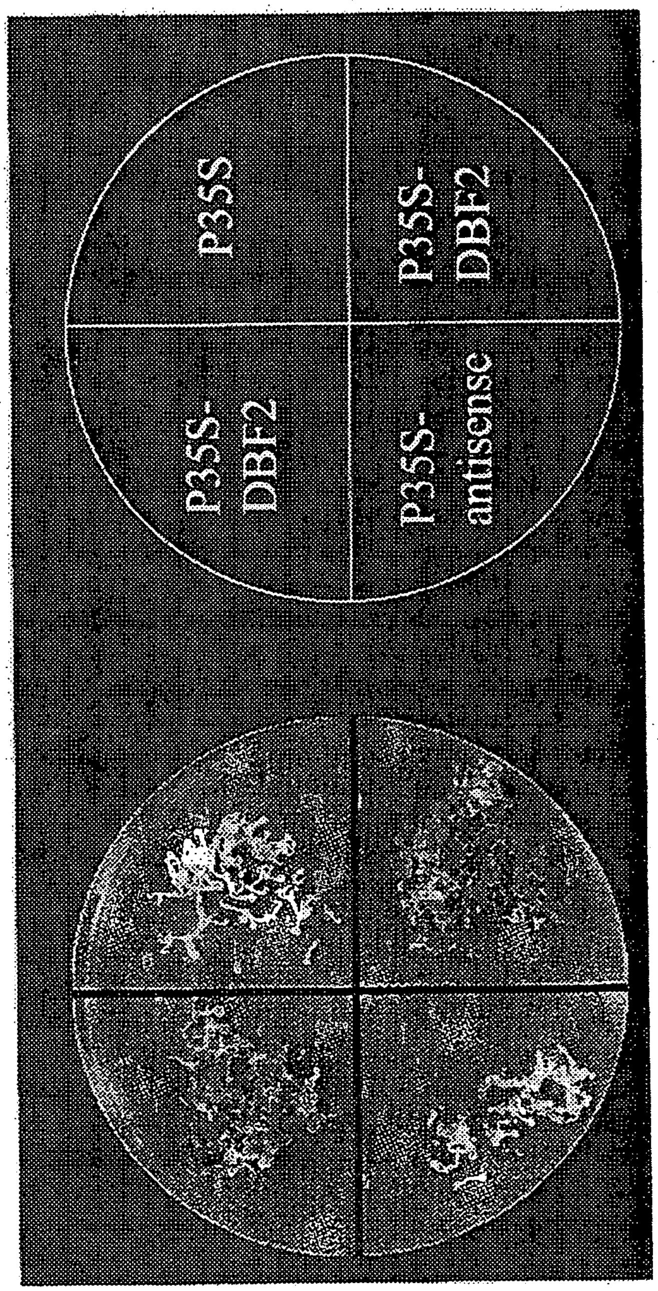
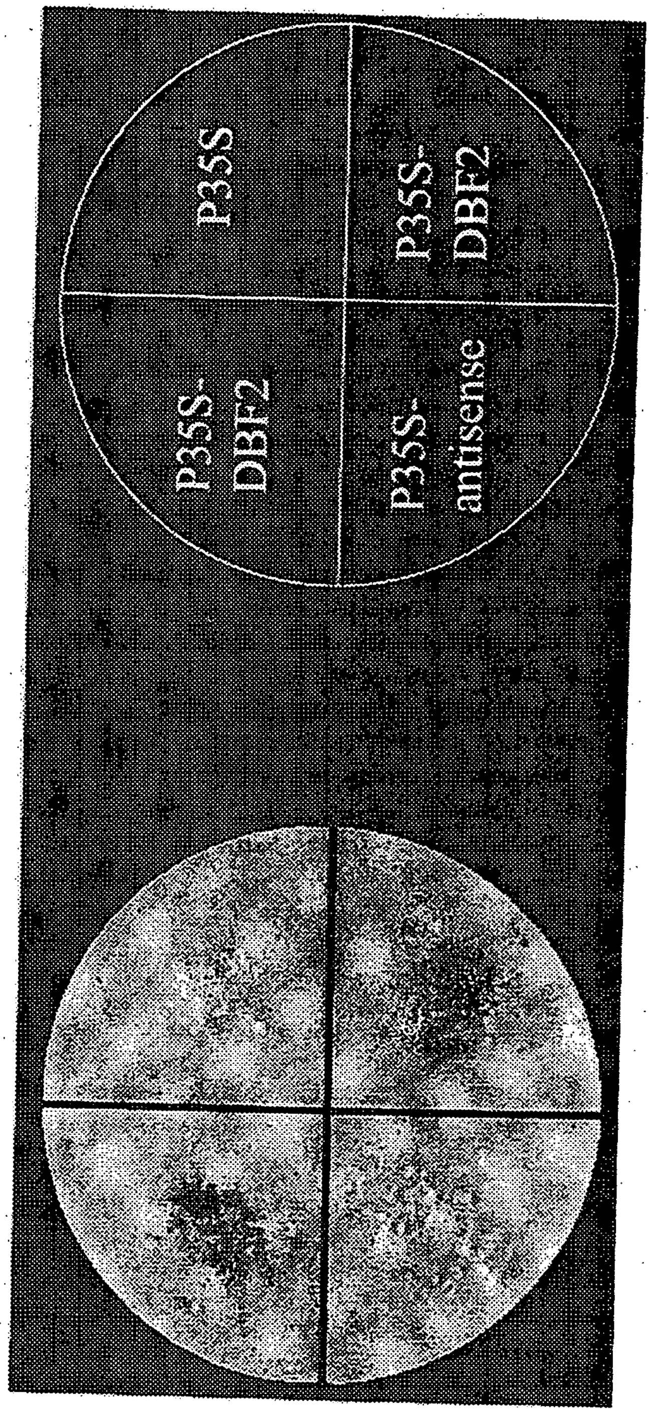


FIGURE 7



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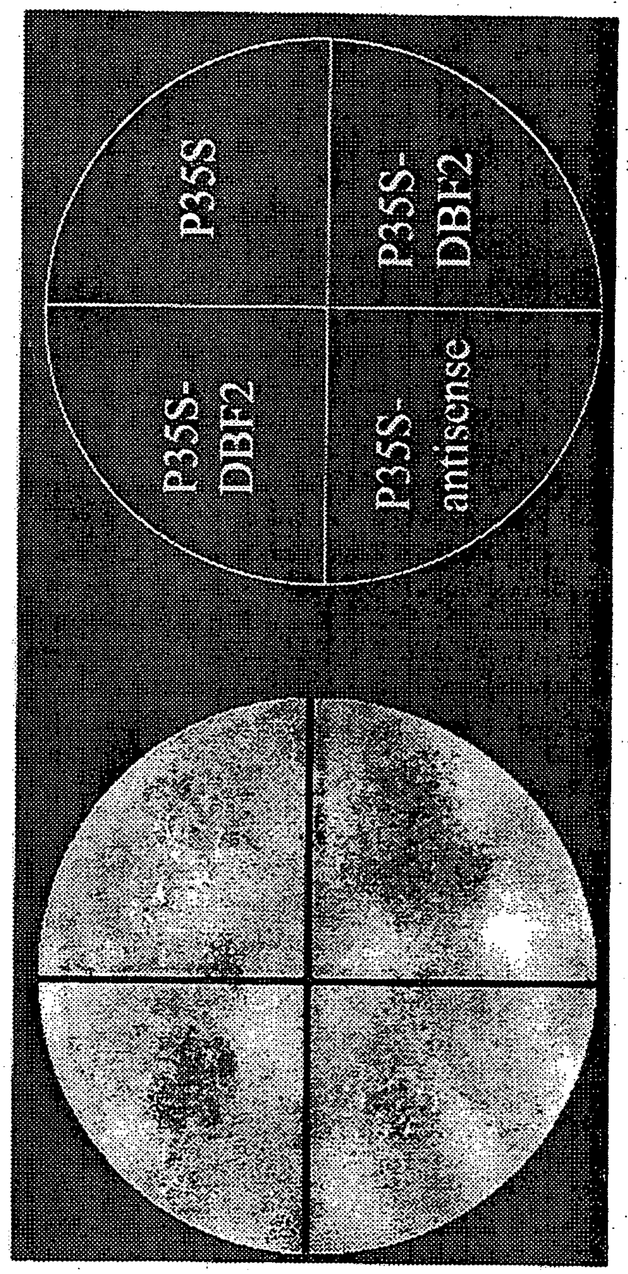


FIGURE 9

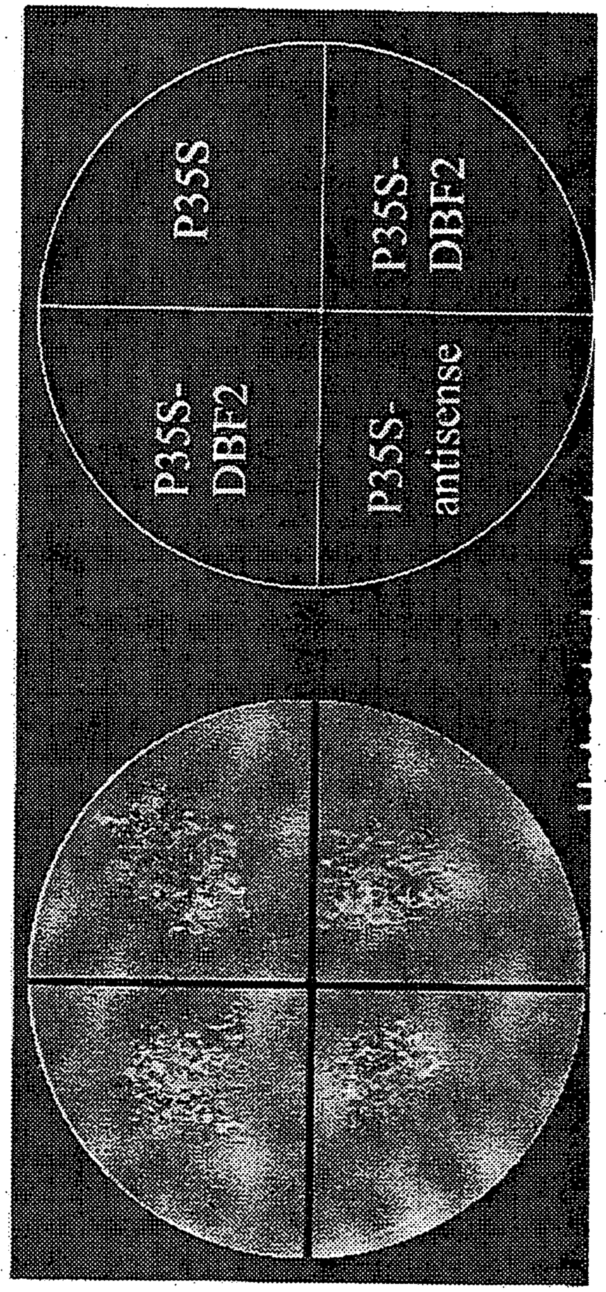


FIGURE 10

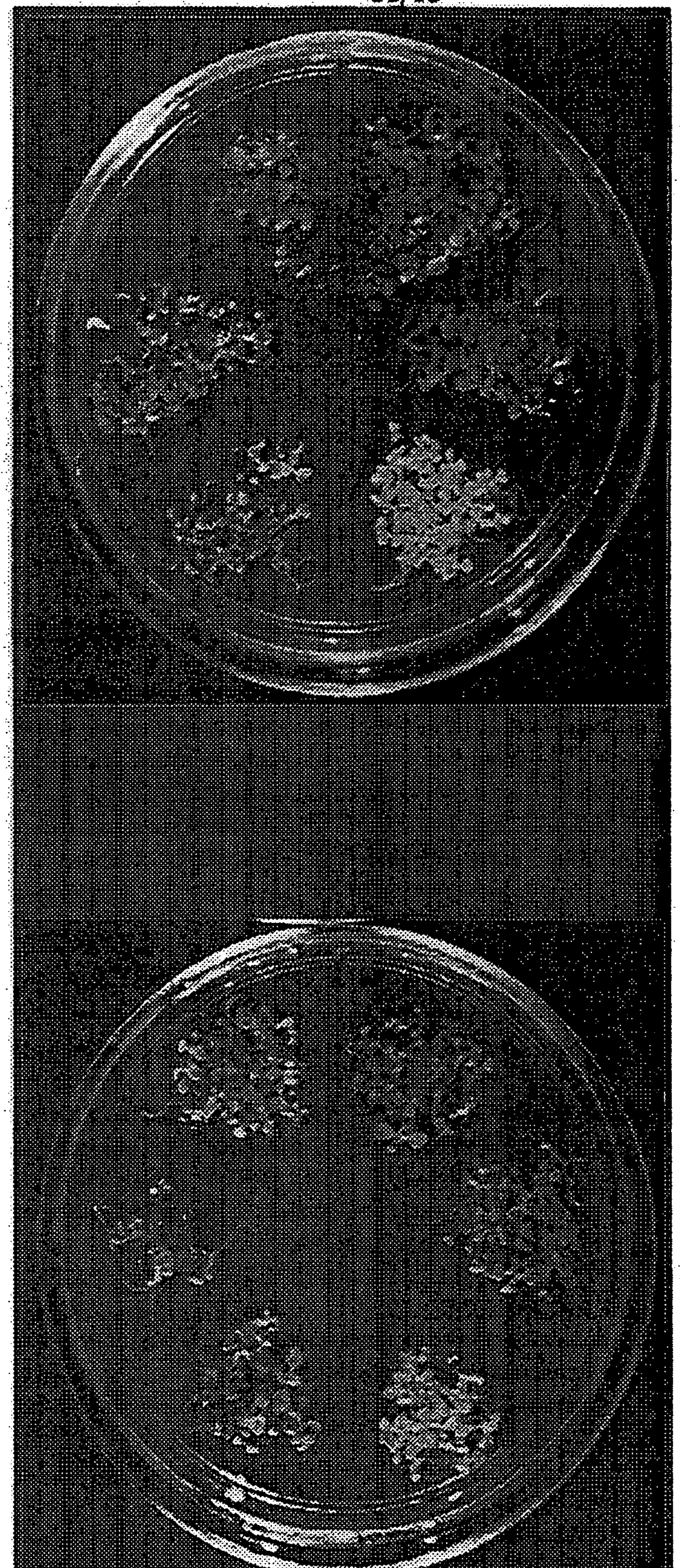


FIGURE 11

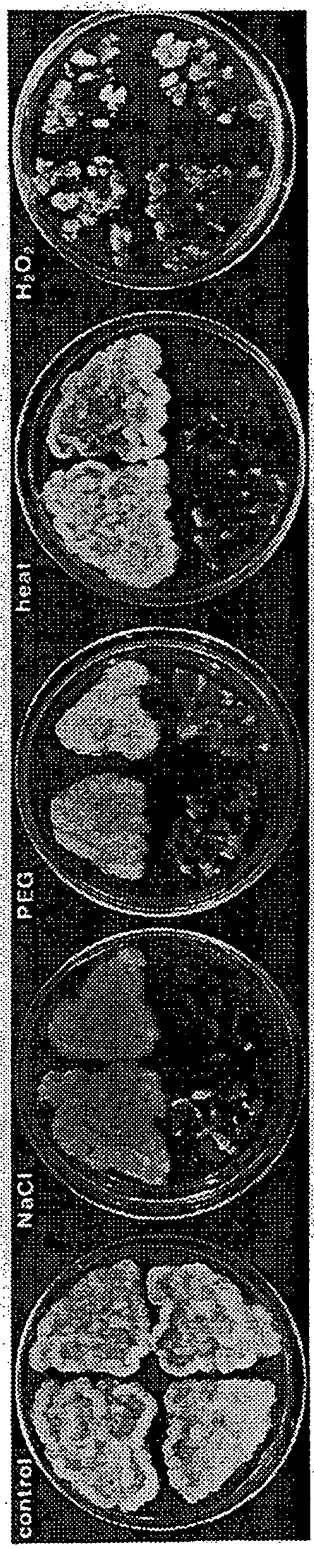


FIGURE 12A

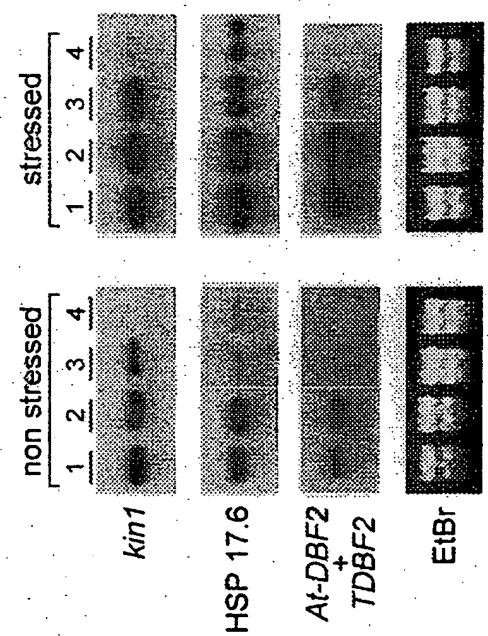
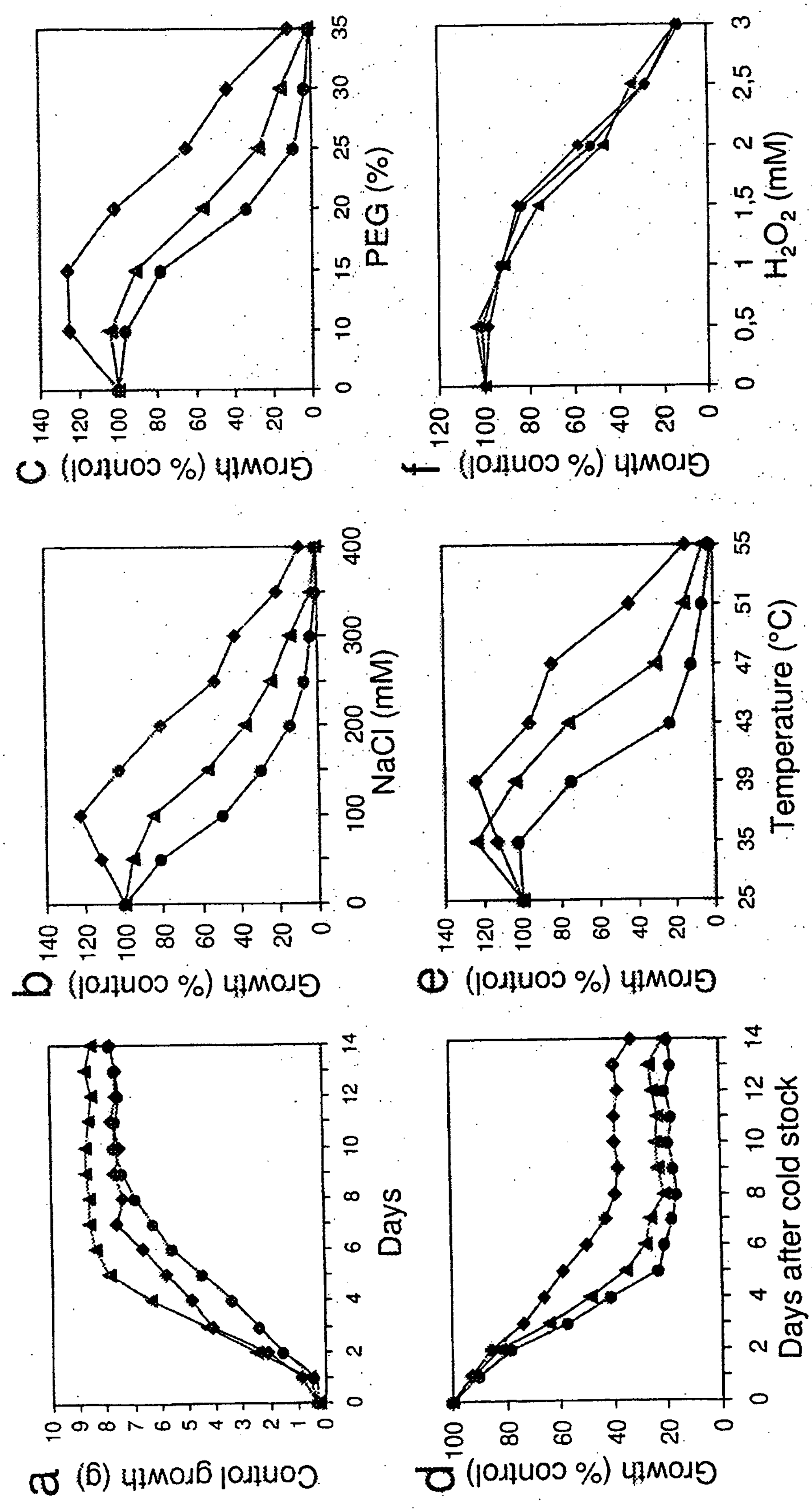


FIGURE 12c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Control growth (g)
Days
b
Growth (% control)
NaCl (mM)
c
Growth (% control)
PEG (%)
d
Growth (% control)
Days after cold stock
e
Growth (% control)
Temperature (°C)
f
Growth (% control)
H_2O_2 (mM)

FIGURE 12B

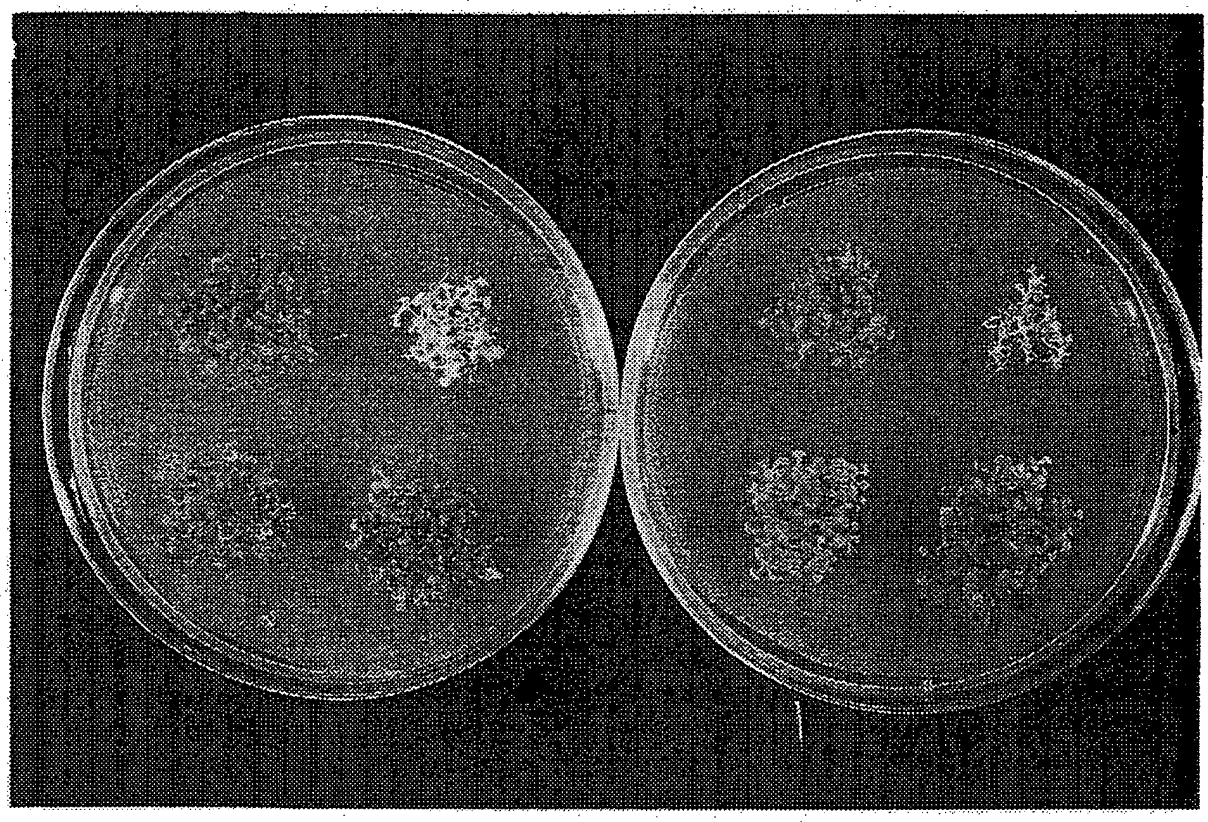

FIGURE 13

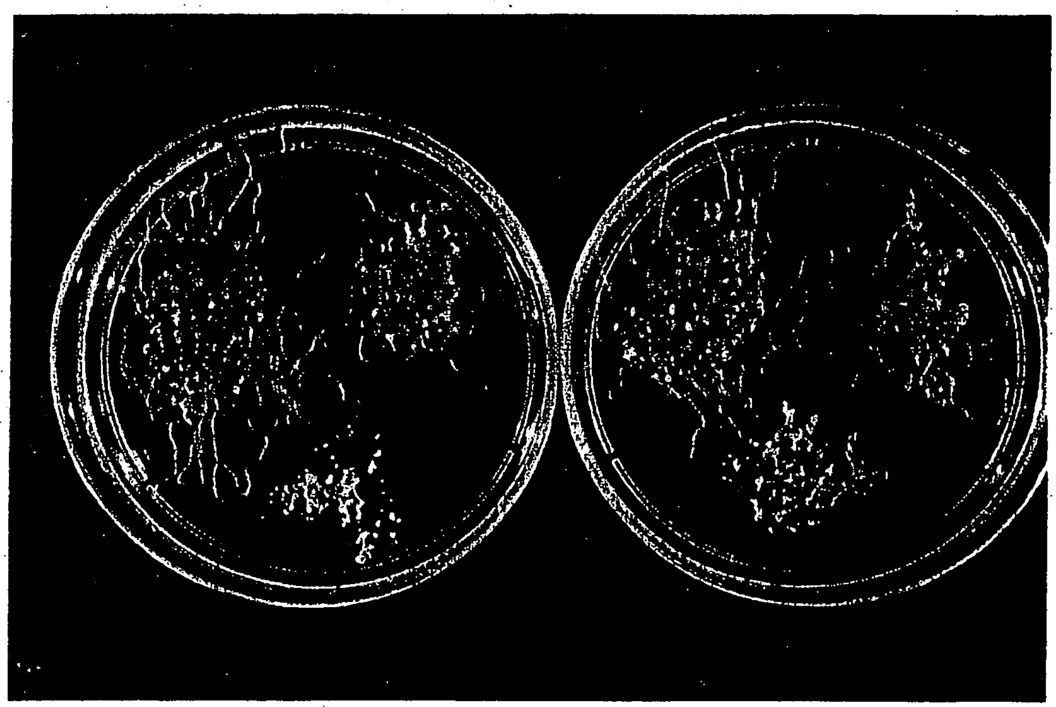

FIGURE 14

SEQUENCE LISTING

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Ser Asn Ser Pro Pro Val Ser Pro Ala Ile Phe Tyr Glu Arg Ala Thr
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230                 235                 240                 245

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Lys Ser Gly His Ala Arg Phe Tyr Ile Ser Glu Met Phe Cys Ala Val
            265                 270                 275

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Asn Glu Lys His Leu Leu Ser Lys Thr Asp Ser Thr Ile Ser Asn Glu
        280                 285                 290

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Glu Asp Ser Ser Ile Asn Ile Arg Leu Glu Lys Phe Lys Asp Leu Gly
    295                 300                 305

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310                 315                 320                 325

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gcacgagcaa gaaagttaac acaacagcta aga atg gat ttg gag ttt gga agg 114
Met Asp Leu Glu Phe Gly Arg
1 5

ttt cca ata ttt tca atc ctc gaa gac atg ctt gaa gcc cct gaa gaa 162
Phe Pro Ile Phe Ser Ile Leu Glu Asp Met Leu Glu Ala Pro Glu Glu
10 15 20

caa acc gag aag act cgt aac aac cct tca aga gct tac atg cga gac 210
Gln Thr Glu Lys Thr Arg Asn Asn Pro Ser Arg Ala Tyr Met Arg Asp
25 30 35

gca aag gca atg gct gct aca cca gct gac gtt atc gag cac ccg gat 258
Ala Lys Ala Met Ala Ala Thr Pro Ala Asp Val Ile Glu His Pro Asp
40 45 50 55

gcg tac gtt ttc gcc gtg gac atg cct gga atc aaa gga gat gag att 306
Ala Tyr Val Phe Ala Val Asp Met Pro Gly Ile Lys Gly Asp Glu Ile
60 65 70

cag gtc cag ata gag aac gag aac gtg ctt gtg gtg agt ggc aaa aga 354
Gln Val Gln Ile Glu Asn Glu Asn Val Leu Val Val Ser Gly Lys Arg
75 80 85

cag agg gac aac aag gag aat gaa ggt gtg aag ttt gtg agg atg gag 402
Gln Arg Asp Asn Lys Glu Asn Glu Gly Val Lys Phe Val Arg Met Glu
90 95 100

agg agg atg ggg aag ttt atg agg aag ttt cag tta cct gat aat gca 450
Arg Arg Met Gly Lys Phe Met Arg Lys Phe Gln Leu Pro Asp Asn Ala
105 110 115

gat ttg gag aag atc tct gcg gct tgt aat gac ggt gtg ttg aaa gtg 498
Asp Leu Glu Lys Ile Ser Ala Ala Cys Asn Asp Gly Val Leu Lys Val
120 125 130 135

act att ccg aaa ctt cct cct cct gag cca aag aaa cca aag act ata 546
Thr Ile Pro Lys Leu Pro Pro Pro Glu Pro Lys Lys Pro Lys Thr Ile
140 145 150

caa gtt caa gtc gct tga gtttgtttgt gatccgtgtt tttgtgtttt 594
Gln Val Gln Val Ala
155

aatgaatgta atcgataagc aactacctct tggtgttcgt tgtaaaatga aataaaaata 654

gttttctctg ttcataaaaa aaaaaaaaaa aaaactcgag c 695

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<212> PRT
<213> Arabidopsis thaliana

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 1               5                  10                  15

Met Leu Glu Ala Pro Glu Glu Gln Thr Glu Lys Thr Arg Asn Asn Pro
            20                  25                  30

Ser Arg Ala Tyr Met Arg Asp Ala Lys Ala Met Ala Ala Thr Pro Ala
        35                  40                  45

Asp Val Ile Glu His Pro Asp Ala Tyr Val Phe Ala Val Asp Met Pro
    50                  55                  60

Gly Ile Lys Gly Asp Glu Ile Gln Val Gln Ile Glu Asn Glu Asn Val
65                  70                  75                  80

Leu Val Val Ser Gly Lys Arg Gln Arg Asp Asn Lys Glu Asn Glu Gly
                85                  90                  95

Val Lys Phe Val Arg Met Glu Arg Arg Met Gly Lys Phe Met Arg Lys
            100                 105                 110

Phe Gln Leu Pro Asp Asn Ala Asp Leu Glu Lys Ile Ser Ala Ala Cys
        115                 120                 125

Asn Asp Gly Val Leu Lys Val Thr Ile Pro Lys Leu Pro Pro Pro Glu
    130                 135                 140

Pro Lys Lys Pro Lys Thr Ile Gln Val Gln Val Ala
145                 150                 155
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<220>
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<222> (133)..(1083)

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ttgccatttc tcagattccg gggaaagaaa aaaaaaacct agaaaagtgt tttctccgtt 120

ttccaatcat cc atg agt ccg gac aat aaa ctg ctt ccg aag cgg atc atc 171
              Met Ser Pro Asp Asn Lys Leu Leu Pro Lys Arg Ile Ile
               1               5                  10
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ctt gta cgg cac ggt gaa tcg gaa ggg aat ctc gac acg gcg gcg tat   219
Leu Val Arg His Gly Glu Ser Glu Gly Asn Leu Asp Thr Ala Ala Tyr
     15                  20                  25

aca acg acg ccg gat cat aag atc cag tta acg gat tcc ggt ttg ctt   267
Thr Thr Thr Pro Asp His Lys Ile Gln Leu Thr Asp Ser Gly Leu Leu
 30                  35                  40                  45

cag gcg cag gaa gcc gga gct cgt ctc cac gct ttg atc tct tct aat   315
Gln Ala Gln Glu Ala Gly Ala Arg Leu His Ala Leu Ile Ser Ser Asn
                 50                  55                  60

cct tct tca ccg gag tgg cgt gtg tac ttc tac gtt tcg ccg tac gat   363
Pro Ser Ser Pro Glu Trp Arg Val Tyr Phe Tyr Val Ser Pro Tyr Asp
             65                  70                  75

cgg act cga tct acg ctc cgg gag atc gga cgg tcg ttc tcg cgt cgc   411
Arg Thr Arg Ser Thr Leu Arg Glu Ile Gly Arg Ser Phe Ser Arg Arg
         80                  85                  90

cgt gtg att ggt gtt cgc gaa gaa tgt cgg att agg gaa cag gat ttt   459
Arg Val Ile Gly Val Arg Glu Glu Cys Arg Ile Arg Glu Gln Asp Phe
     95                 100                 105

ggg aat ttt cag gtt aaa gag cga atg aga gca acg aaa aag gtc aga   507
Gly Asn Phe Gln Val Lys Glu Arg Met Arg Ala Thr Lys Lys Val Arg
110                 115                 120                 125

gag aga ttt ggc cgc ttt ttt tac cgg ttc ccg gag gga gaa tcc gcc   555
Glu Arg Phe Gly Arg Phe Phe Tyr Arg Phe Pro Glu Gly Glu Ser Ala
                130                 135                 140

gcc gat gtc ttc gat cgc gtc tcc agt ttt ctc gag tct cta tgg aga   603
Ala Asp Val Phe Asp Arg Val Ser Ser Phe Leu Glu Ser Leu Trp Arg
            145                 150                 155

gac att gac atg aac aga ctg cac atc aac ccg tct cat gag cta aac   651
Asp Ile Asp Met Asn Arg Leu His Ile Asn Pro Ser His Glu Leu Asn
        160                 165                 170

ttt gtg att gtc tca cat ggc tta aca tcg cgt gtg ttt ctg atg aaa   699
Phe Val Ile Val Ser His Gly Leu Thr Ser Arg Val Phe Leu Met Lys
    175                 180                 185

tgg ttt aag tgg tca gtg gaa cag ttc gag gga cta aac aat cca ggg   747
Trp Phe Lys Trp Ser Val Glu Gln Phe Glu Gly Leu Asn Asn Pro Gly
190                 195                 200                 205

aac agt gag atc aga gtg atg gaa tta gga caa ggc ggt gat tac agc   795
Asn Ser Glu Ile Arg Val Met Glu Leu Gly Gln Gly Gly Asp Tyr Ser
                210                 215                 220

ttg gcg att cat cac aca gag gaa gag tta gcc aca tgg gga ctg tca   843
Leu Ala Ile His His Thr Glu Glu Glu Leu Ala Thr Trp Gly Leu Ser
            225                 230                 235

cca gag atg att gca gat caa aag tgg cgg gct aac gcg cat aaa ggc   891
```

```
Pro Glu Met Ile Ala Asp Gln Lys Trp Arg Ala Asn Ala His Lys Gly
        240                 245                 250

gaa tgg aaa gaa gat tgt aag tgg tat ttt ggt gat ttc ttc gac cat      939
Glu Trp Lys Glu Asp Cys Lys Trp Tyr Phe Gly Asp Phe Phe Asp His
    255                 260                 265

atg gca gat tcc gat aaa gag tgc gag act gag gcc act gaa gat aga      987
Met Ala Asp Ser Asp Lys Glu Cys Glu Thr Glu Ala Thr Glu Asp Arg
270                 275                 280                 285

gaa gaa gaa gaa gaa gaa gag ggg aaa agg gta aat ctg cta acg agt     1035
Glu Glu Glu Glu Glu Glu Glu Gly Lys Arg Val Asn Leu Leu Thr Ser
                290                 295                 300

tca gaa tat agc aat gag cca gag tta tac aat gga caa tgc tgc tga     1083
Ser Glu Tyr Ser Asn Glu Pro Glu Leu Tyr Asn Gly Gln Cys Cys
            305                 310                 315

tactatttta cagaacaaaa gcatacatga gaagaaacgt ttaactaaag aattcagaag 1143

atttgatttt gataaaaact tgtaccaatt tactgattaa gctttctggt gtcttagttt 1203

gtagcttttg gtttgtggaa aagtgttgta cacatcgtta taacaccagg aaacattaca 1263

ggaaatttga aagattcatt ttattgtgac aaaaaaaaaa aaaaaaaa                1311


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<212> PRT
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1               5                   10                  15

His Gly Glu Ser Glu Gly Asn Leu Asp Thr Ala Ala Tyr Thr Thr Thr
            20                  25                  30

Pro Asp His Lys Ile Gln Leu Thr Asp Ser Gly Leu Leu Gln Ala Gln
        35                  40                  45

Glu Ala Gly Ala Arg Leu His Ala Leu Ile Ser Ser Asn Pro Ser Ser
    50                  55                  60

Pro Glu Trp Arg Val Tyr Phe Tyr Val Ser Pro Tyr Asp Arg Thr Arg
65                  70                  75                  80

Ser Thr Leu Arg Glu Ile Gly Arg Ser Phe Ser Arg Arg Arg Val Ile
                85                  90                  95

Gly Val Arg Glu Glu Cys Arg Ile Arg Glu Gln Asp Phe Gly Asn Phe
            100                 105                 110

Gln Val Lys Glu Arg Met Arg Ala Thr Lys Lys Val Arg Glu Arg Phe
        115                 120                 125
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Gly Arg Phe Phe Tyr Arg Phe Pro Glu Gly Glu Ser Ala Ala Asp Val
130 135 140

Phe Asp Arg Val Ser Ser Phe Leu Glu Ser Leu Trp Arg Asp Ile Asp
145 150 155 160

Met Asn Arg Leu His Ile Asn Pro Ser His Glu Leu Asn Phe Val Ile
165 170 175

Val Ser His Gly Leu Thr Ser Arg Val Phe Leu Met Lys Trp Phe Lys
180 185 190

Trp Ser Val Glu Gln Phe Glu Gly Leu Asn Asn Pro Gly Asn Ser Glu
195 200 205

Ile Arg Val Met Glu Leu Gly Gln Gly Gly Asp Tyr Ser Leu Ala Ile
210 215 220

His His Thr Glu Glu Glu Leu Ala Thr Trp Gly Leu Ser Pro Glu Met
225 230 235 240

Ile Ala Asp Gln Lys Trp Arg Ala Asn Ala His Lys Gly Glu Trp Lys
245 250 255

Glu Asp Cys Lys Trp Tyr Phe Gly Asp Phe Phe Asp His Met Ala Asp
260 265 270

Ser Asp Lys Glu Cys Glu Thr Glu Ala Thr Glu Asp Arg Glu Glu Glu
275 280 285

Glu Glu Glu Glu Gly Lys Arg Val Asn Leu Leu Thr Ser Ser Glu Tyr
290 295 300

Ser Asn Glu Pro Glu Leu Tyr Asn Gly Gln Cys Cys
305 310 315

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<211> 863
<212> DNA
<213> Arabidopsis thaliana

<220>
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<222> (19)..(837)

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1 5 10

gta gct ata ata acc gga gga gca aga ggg ata gga gcg gcc acg gcg 99
Val Ala Ile Ile Thr Gly Gly Ala Arg Gly Ile Gly Ala Ala Thr Ala
15 20 25

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aga ttg ttc aca gag aat ggc gcg tat gtg ata gtc gcg gat atc ctt   147
Arg Leu Phe Thr Glu Asn Gly Ala Tyr Val Ile Val Ala Asp Ile Leu
        30                  35                  40

gat aat gaa ggc atc ctt gtg gcg gaa tcg atc ggt ggg tgt tac gtt   195
Asp Asn Glu Gly Ile Leu Val Ala Glu Ser Ile Gly Gly Cys Tyr Val
    45                  50                  55

cat tgt gac gta tcg aag gag gct gat gtt gag gcg gca gtg gag cta   243
His Cys Asp Val Ser Lys Glu Ala Asp Val Glu Ala Ala Val Glu Leu
60                  65                  70                  75

gca atg aga cgt aaa ggt aga cta gat gtg atg ttc aac aat gcc ggg   291
Ala Met Arg Arg Lys Gly Arg Leu Asp Val Met Phe Asn Asn Ala Gly
                80                  85                  90

atg tcg ctt aac gaa ggt agt atc atg ggg atg gac gtg gac atg gtt   339
Met Ser Leu Asn Glu Gly Ser Ile Met Gly Met Asp Val Asp Met Val
            95                  100                 105

aac aaa ctt gtc tcg gtt aat gtc aat ggt gtt ttg cat ggt atc aaa   387
Asn Lys Leu Val Ser Val Asn Val Asn Gly Val Leu His Gly Ile Lys
        110                 115                 120

cat gcc gct aag gcc atg atc aaa ggg gga cga gga ggc tcg ata ata   435
His Ala Ala Lys Ala Met Ile Lys Gly Gly Arg Gly Gly Ser Ile Ile
    125                 130                 135

tgc aca tcg agc tca tca ggg cta atg gga gga ctt gga gga cat gcg   483
Cys Thr Ser Ser Ser Ser Gly Leu Met Gly Gly Leu Gly Gly His Ala
140                 145                 150                 155

tat acg ctc tcc aaa gga ggc atc aac ggg gtg gtg agg aca acg gag   531
Tyr Thr Leu Ser Lys Gly Gly Ile Asn Gly Val Val Arg Thr Thr Glu
                160                 165                 170

tgc gag ctt ggg tct cac ggc atc cgt gtg aat agc atc tct cct cat   579
Cys Glu Leu Gly Ser His Gly Ile Arg Val Asn Ser Ile Ser Pro His
            175                 180                 185

gga gtt ccc act gac atc ttg gtt aat gcg tac cgt aag ttc ctt aac   627
Gly Val Pro Thr Asp Ile Leu Val Asn Ala Tyr Arg Lys Phe Leu Asn
        190                 195                 200

aat gac aaa ctc aac gtc gct gag gtc acc gac att att gct gag aaa   675
Asn Asp Lys Leu Asn Val Ala Glu Val Thr Asp Ile Ile Ala Glu Lys
    205                 210                 215

ggg agt ttg ctg acc gga aga gcc ggt act gtg gag gac gta gct caa   723
Gly Ser Leu Leu Thr Gly Arg Ala Gly Thr Val Glu Asp Val Ala Gln
220                 225                 230                 235

gca gct ttg ttt ctt gca agc caa gaa tcg tcg ggg ttc att acc gga   771
Ala Ala Leu Phe Leu Ala Ser Gln Glu Ser Ser Gly Phe Ile Thr Gly
                240                 245                 250

cat aac ttg gtt gtt gat ggt ggt tac aca tct gcc act agt act atg   819
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His Asn Leu Val Val Asp Gly Gly Tyr Thr Ser Ala Thr Ser Thr Met
            255                 260                 265

aga ttt atc tac aac tag ttttcgtttg gtggtgtttc cttttc              863
Arg Phe Ile Tyr Asn
        270


<210> 8
<211> 272
<212> PRT
<213> Arabidopsis thaliana

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Met Ala Asn Ser Asp Lys Arg Leu Phe Glu Lys Val Ala Ile Ile Thr
1               5                   10                  15

Gly Gly Ala Arg Gly Ile Gly Ala Ala Thr Ala Arg Leu Phe Thr Glu
            20                  25                  30

Asn Gly Ala Tyr Val Ile Val Ala Asp Ile Leu Asp Asn Glu Gly Ile
        35                  40                  45

Leu Val Ala Glu Ser Ile Gly Gly Cys Tyr Val His Cys Asp Val Ser
    50                  55                  60

Lys Glu Ala Asp Val Glu Ala Ala Val Glu Leu Ala Met Arg Arg Lys
65                  70                  75                  80

Gly Arg Leu Asp Val Met Phe Asn Asn Ala Gly Met Ser Leu Asn Glu
                85                  90                  95

Gly Ser Ile Met Gly Met Asp Val Asp Met Val Asn Lys Leu Val Ser
            100                 105                 110

Val Asn Val Asn Gly Val Leu His Gly Ile Lys His Ala Ala Lys Ala
        115                 120                 125

Met Ile Lys Gly Gly Arg Gly Gly Ser Ile Ile Cys Thr Ser Ser Ser
    130                 135                 140

Ser Gly Leu Met Gly Gly Leu Gly Gly His Ala Tyr Thr Leu Ser Lys
145                 150                 155                 160

Gly Gly Ile Asn Gly Val Val Arg Thr Thr Glu Cys Glu Leu Gly Ser
                165                 170                 175

His Gly Ile Arg Val Asn Ser Ile Ser Pro His Gly Val Pro Thr Asp
            180                 185                 190

Ile Leu Val Asn Ala Tyr Arg Lys Phe Leu Asn Asn Asp Lys Leu Asn
        195                 200                 205

Val Ala Glu Val Thr Asp Ile Ile Ala Glu Lys Gly Ser Leu Leu Thr
    210                 215                 220

Gly Arg Ala Gly Thr Val Glu Asp Val Ala Gln Ala Ala Leu Phe Leu
```

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ttgttgtttt ttttttata gtatgacaca catgtgttct aaaaatcgga cgttcaaatg 414

atataatcga ttgtttagac gtccgaccgt atattatttt agtgatatca gccaaatcag 474

attaagtaat catcaacaaa atgattgatc agatctatca atacaagtgt attttttttt 534

cacatacaaa aaaattatct caccgacgaa aaaaaaataa aaaattatta tgtagatcca 594

tcgaacaaaa ggcttgaata tcggaagtca cttaaaagtg taataatcga ataaatatta 654

gtggataaaa tgaaatttat ctacaaccct actctccgac atgttactgt ttgcgtcatc 714

aaatctaaag ccttttggc aaataatggt cggaagacta ctcgtgtcgg gatggaccac 774

ccggatccga tcaggaaacg ggttttgata tgtttcgggt tacgacaaaa aattagggct 834

ttttatcaaa tcaatcagtt ggtagtaaaa ttttgtggat tgttcttgtc gattccgttt 894

gattgttgac caaatttctt cctaggattt tgttgataat cgatcgtata atggtgattg 954

cag tat cgt cct tca agc gcg tac aac gcc cca ttc tac acc aca aac     1002
    Tyr Arg Pro Ser Ser Ala Tyr Asn Ala Pro Phe Tyr Thr Thr Asn
                    10                  15                  20

ggt ggt gct cca gtc tcc aac aac atc tct tcc ctc acc atc gga gaa     1050
Gly Gly Ala Pro Val Ser Asn Asn Ile Ser Ser Leu Thr Ile Gly Glu
                25                  30                  35

aga g gtatcgtaac cctgaatttc aagagtctat caataagaat cggaacttgt        1104
Arg G

tggatttatg aaagagataa aactgagata tagagtctaa gctgagatct gttcgtgaag 1164

cgtgatgtga ttatttttaa catgtgttac ttcgtaatgg gcag gt ccg gtt ctt     1219
                                                 ly Pro Val Leu
                                                            40

ctt gag gat tat cat ttg atc gag aag gtt gct aat ttc acc aga gag     1267
Leu Glu Asp Tyr His Leu Ile Glu Lys Val Ala Asn Phe Thr Arg Glu
            45                  50                  55

agg atc cct gag aga gtg gtt cat gct aga gga atc agt gct aag ggt     1315
Arg Ile Pro Glu Arg Val Val His Ala Arg Gly Ile Ser Ala Lys Gly
        60                  65                  70

ttc ttt gaa gtc acc cat gac att tca aac ctc act tgt gct gat ttt     1363
Phe Phe Glu Val Thr His Asp Ile Ser Asn Leu Thr Cys Ala Asp Phe
    75                  80                  85

ctc aga gcc cct ggt gtt caa act ccg gtt att gtc cgt ttc tca acg     1411
Leu Arg Ala Pro Gly Val Gln Thr Pro Val Ile Val Arg Phe Ser Thr
 90                  95                 100                 105

gtt gtt cac gga cgt gcc agt cct gaa acc atg agg gat att cgt ggt     1459
Val Val His Gly Arg Ala Ser Pro Glu Thr Met Arg Asp Ile Arg Gly
                110                 115                 120
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ttt gct gtc aag ttt tac acc aga gag gtataagaaa gattcaaagt 1506
Phe Ala Val Lys Phe Tyr Thr Arg Glu
125 130

ttccattttt aatcgtcttt tagcttcttt agaatcagga ctgattttg tcttgttact 1566

gttatgatca g gga aac ttt gat ctt gtt ggg aac aac act ccg gtg ttc 1616
Gly Asn Phe Asp Leu Val Gly Asn Asn Thr Pro Val Phe
135 140

ttc atc cgt gat ggg att cag ttc ccg gat gtt gtc cac gcg ttg aaa 1664
Phe Ile Arg Asp Gly Ile Gln Phe Pro Asp Val Val His Ala Leu Lys
145 150 155

cct aac cga aaa aca aac atc caa gag tac tgg agg att ctg gac tac 1712
Pro Asn Arg Lys Thr Asn Ile Gln Glu Tyr Trp Arg Ile Leu Asp Tyr
160 165 170 175

atg tcc cac ttg cct gag agt ttg ctc aca tgg tgc tgg atg ttt gat 1760
Met Ser His Leu Pro Glu Ser Leu Leu Thr Trp Cys Trp Met Phe Asp
180 185 190

gat gtt ggt att cca caa gat tac agg cat atg gag ggt ttc ggt gtc 1808
Asp Val Gly Ile Pro Gln Asp Tyr Arg His Met Glu Gly Phe Gly Val
195 200 205

cac acc tac act ctt att gcc aaa tct gga aaa gtt ctc ttt gtg aag 1856
His Thr Tyr Thr Leu Ile Ala Lys Ser Gly Lys Val Leu Phe Val Lys
210 215 220

ttc cac tgg aaa cca act tgt ggg atc aag aat ctg act gat gaa gag 1904
Phe His Trp Lys Pro Thr Cys Gly Ile Lys Asn Leu Thr Asp Glu Glu
225 230 235

gcc aag gtt gtt gga gga gcc aat cac agc cac gcc act aag gat ctc 1952
Ala Lys Val Val Gly Gly Ala Asn His Ser His Ala Thr Lys Asp Leu
240 245 250 255

cac gat gcc att gca tct ggc aac tac ccc gag tgg aaa ctt ttc atc 2000
His Asp Ala Ile Ala Ser Gly Asn Tyr Pro Glu Trp Lys Leu Phe Ile
260 265 270

cag acc atg gat cct gca gat gag gat aag ttt gac ttt gac cca ctt 2048
Gln Thr Met Asp Pro Ala Asp Glu Asp Lys Phe Asp Phe Asp Pro Leu
275 280 285

gat gtg acc aag atc tgg cct gag gat att ttg cct ctg caa ccg gtt 2096
Asp Val Thr Lys Ile Trp Pro Glu Asp Ile Leu Pro Leu Gln Pro Val
290 295 300

ggt cgc ttg gtt ctg aac agg acc att gac aac ttc ttc aat gaa act 2144
Gly Arg Leu Val Leu Asn Arg Thr Ile Asp Asn Phe Phe Asn Glu Thr
305 310 315

gag cag ctt gcg ttc aac ccg ggt ctt gtg gtt cct gga atc tac tac 2192
Glu Gln Leu Ala Phe Asn Pro Gly Leu Val Val Pro Gly Ile Tyr Tyr

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320                 325                 330                 335

tca gac gac aag ctg ctc cag tgt agg atc ttt gct tat ggt gac act    2240
Ser Asp Asp Lys Leu Leu Gln Cys Arg Ile Phe Ala Tyr Gly Asp Thr
                340                 345                 350

cag aga cat cgc ctt gga ccg aat tat ttg cag ctt cca gtc aat gct    2288
Gln Arg His Arg Leu Gly Pro Asn Tyr Leu Gln Leu Pro Val Asn Ala
            355                 360                 365

ccc aaa tgt gct cac cac aac aat cac cat gaa ggt ttt atg aac ttc    2336
Pro Lys Cys Ala His His Asn Asn His His Glu Gly Phe Met Asn Phe
        370                 375                 380

atg cac aga gat gag gag gtacgtctta gtacaccact tgagctacca           2384
Met His Arg Asp Glu Glu
    385

ttgttagtct ttttacttgg aatcaaaatt ctcatttggt ttgtactttt tacag atc   2442
                                                             Ile
                                                             390

aat tac tac ccc tca aag ttt gat cct gtc cgc tgc gct gag aaa gtt    2490
Asn Tyr Tyr Pro Ser Lys Phe Asp Pro Val Arg Cys Ala Glu Lys Val
                395                 400                 405

ccc acc cct aca aac tcc tac act gga att cga aca aag gtccgattcc     2539
Pro Thr Pro Thr Asn Ser Tyr Thr Gly Ile Arg Thr Lys
            410                 415

tgccatgcct tctctaaatc ttcaaatcct aaactcaagt ttattagaat attggtgcta 2599

agaaaacctt ttaattgcta atgttgcag tgc gtc atc aag aaa gag aac aac    2652
                                Cys Val Ile Lys Lys Glu Asn Asn
                                420                 425

ttc aaa cag gct gga gac agg tac aga tca tgg gca cca gac agg caa    2700
Phe Lys Gln Ala Gly Asp Arg Tyr Arg Ser Trp Ala Pro Asp Arg Gln
        430                 435                 440

gac agg ttt gtt aag aga tgg gtg gag att cta tcg gag cca cgt ctc    2748
Asp Arg Phe Val Lys Arg Trp Val Glu Ile Leu Ser Glu Pro Arg Leu
    445                 450                 455

acc cac gag atc cgc ggc atc tgg acc tct tac tgg ctc aag            2790
Thr His Glu Ile Arg Gly Ile Trp Thr Ser Tyr Trp Leu Lys
460                 465                 470

gtcagaacca aaaaaacact cggtcaaatt tctacgtcct ttttaccaag tttcagcaaa 2850

ctaaaacatt atttatctct ctgtatctct cag gct gat cga tcc ttg gga cag   2904
                                    Ala Asp Arg Ser Leu Gly Gln
                                        475                 480

aaa ctc gca agc cgt ctg aac gtg agg cca agc atc tag aggccaatct     2953
Lys Leu Ala Ser Arg Leu Asn Val Arg Pro Ser Ile
                485                 490
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ccatataagc tcagtctatg tgaggtacaa tcaatctcat cgatctatca tcgcttggtc 3013

gttaaatccg tcaaaaagat aatcacatgt gttgttgttt cttgtctata taataataat 3073

gcttgtaatc ccaaaaactc atgtttcctt cctt 3107

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<212> PRT
<213> Arabidopsis thaliana

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20 25 30

Leu Thr Ile Gly Glu Arg Gly Pro Val Leu Leu Glu Asp Tyr His Leu
35 40 45

Ile Glu Lys Val Ala Asn Phe Thr Arg Glu Arg Ile Pro Glu Arg Val
50 55 60

Val His Ala Arg Gly Ile Ser Ala Lys Gly Phe Phe Glu Val Thr His
65 70 75 8

Asp Ile Ser Asn Leu Thr Cys Ala Asp Phe Leu Arg Ala Pro Gly Val
85 90 95

Gln Thr Pro Val Ile Val Arg Phe Ser Thr Val Val His Gly Arg Ala
100 105 110

Ser Pro Glu Thr Met Arg Asp Ile Arg Gly Phe Ala Val Lys Phe Tyr
115 120 125

Thr Arg Glu Gly Asn Phe Asp Leu Val Gly Asn Asn Thr Pro Val Phe
130 135 140

Phe Ile Arg Asp Gly Ile Gln Phe Pro Asp Val Val His Ala Leu Lys
145 150 155 16

Pro Asn Arg Lys Thr Asn Ile Gln Glu Tyr Trp Arg Ile Leu Asp Tyr
165 170 175

Met Ser His Leu Pro Glu Ser Leu Leu Thr Trp Cys Trp Met Phe Asp
180 185 190

Asp Val Gly Ile Pro Gln Asp Tyr Arg His Met Glu Gly Phe Gly Val
195 200 205

His Thr Tyr Thr Leu Ile Ala Lys Ser Gly Lys Val Leu Phe Val Lys
210 215 220

Phe His Trp Lys Pro Thr Cys Gly Ile Lys Asn Leu Thr Asp Glu Glu

225 230 235 24

Ala Lys Val Val Gly Gly Ala Asn His Ser His Ala Thr Lys Asp Leu
245 250 255

His Asp Ala Ile Ala Ser Gly Asn Tyr Pro Glu Trp Lys Leu Phe Ile
260 265 270

Gln Thr Met Asp Pro Ala Asp Glu Asp Lys Phe Asp Phe Asp Pro Leu
275 280 285

Asp Val Thr Lys Ile Trp Pro Glu Asp Ile Leu Pro Leu Gln Pro Val
290 295 300

Gly Arg Leu Val Leu Asn Arg Thr Ile Asp Asn Phe Phe Asn Glu Thr
305 310 315 32

Glu Gln Leu Ala Phe Asn Pro Gly Leu Val Val Pro Gly Ile Tyr Tyr
325 330 335

Ser Asp Asp Lys Leu Leu Gln Cys Arg Ile Phe Ala Tyr Gly Asp Thr
340 345 350

Gln Arg His Arg Leu Gly Pro Asn Tyr Leu Gln Leu Pro Val Asn Ala
355 360 365

Pro Lys Cys Ala His His Asn Asn His His Glu Gly Phe Met Asn Phe
370 375 380

Met His Arg Asp Glu Glu Ile Asn Tyr Tyr Pro Ser Lys Phe Asp Pro
385 390 395 40

Val Arg Cys Ala Glu Lys Val Pro Thr Pro Thr Asn Ser Tyr Thr Gly
405 410 415

Ile Arg Thr Lys Cys Val Ile Lys Lys Glu Asn Asn Phe Lys Gln Ala
420 425 430

Gly Asp Arg Tyr Arg Ser Trp Ala Pro Asp Arg Gln Asp Arg Phe Val
435 440 445

Lys Arg Trp Val Glu Ile Leu Ser Glu Pro Arg Leu Thr His Glu Ile
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Arg Gly Ile Trp Thr Ser Tyr Trp Leu Lys Ala Asp Arg Ser Leu Gly
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       Met Ala Asp Val Gln Met Ala Asp Ala Glu Thr Phe Ala Phe
         1               5                  10

caa gct gag att aac cag ctt ctt agc ttg atc atc aac acg ttc tac    156
Gln Ala Glu Ile Asn Gln Leu Leu Ser Leu Ile Ile Asn Thr Phe Tyr
 15                  20                  25                  30

agc aac aaa gaa atc ttc ctc cgt gag ctc atc agt aac tct tct gat    204
Ser Asn Lys Glu Ile Phe Leu Arg Glu Leu Ile Ser Asn Ser Ser Asp
                 35                  40                  45

gtaagtttcc cttcaaatct ctctctgact cggtgtgact cgtccgcttc ctattttctt 264

gactgttgtt tgttctttaa ttcctggatt cgttgatagc gttggattcg taggtttagc 324

gttgtgattg cttattcaaa taaatcgtga tttggcttgt gcatcacgtt aagtttagaa 384

ttcttagctt gtgctcgatc ttcatgtgtt gtagttacat atatagaacg gttcttgctt 444

cgatgtagtt tttgatttac cctagaggat tgagtaaagc ttctgattat ctttgtttat 504

atgaacggtt ttgtag gct ctt gac aag att cga ttt gag agc tta acg gat 556
                  Ala Leu Asp Lys Ile Arg Phe Glu Ser Leu Thr Asp
                                  50                  55

aag agc aag ctc gat gga cag cct gaa ctc ttc att aga ttg gtt cct    604
Lys Ser Lys Leu Asp Gly Gln Pro Glu Leu Phe Ile Arg Leu Val Pro
     60                  65                  70

gac aag cct aat aag acg ctc tca att att gac agt ggt att ggc atg    652
Asp Lys Pro Asn Lys Thr Leu Ser Ile Ile Asp Ser Gly Ile Gly Met
 75                  80                  85                  90

acc aaa gca ggtaacgaat caatgcctaa taatctctcg ttggtgagat           701
Thr Lys Ala

gtttagtgta tgtgctgtgg ttatgactct ctattatttt tca gat ttg gtg aac   756
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                                                Asp Leu Val Asn
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Asn Leu Gly Thr Ile Ala Arg Ser Gly Thr Lys Glu Phe Met Glu Ala
        100                 105                 110

ctt caa gct gga gct gat gta agc atg ata gga caa ttt ggt gtt ggt     852
Leu Gln Ala Gly Ala Asp Val Ser Met Ile Gly Gln Phe Gly Val Gly
    115                 120                 125

ttc tac tct gct tat ctt gtt gca gag aag gtt gtt gtc act aca aag     900
Phe Tyr Ser Ala Tyr Leu Val Ala Glu Lys Val Val Val Thr Thr Lys
130                 135                 140                 145

cac aat gat gat gaa caa tac gtt tgg gag tct caa gct ggt ggt tcc     948
His Asn Asp Asp Glu Gln Tyr Val Trp Glu Ser Gln Ala Gly Gly Ser
                150                 155                 160

ttc act gtc act agg gat gtg gat ggg gaa cca ctt ggt aga gga act     996
Phe Thr Val Thr Arg Asp Val Asp Gly Glu Pro Leu Gly Arg Gly Thr
            165                 170                 175

aag atc agc ctc ttc ctt aag gac gat cag gtaaggaatc gtagctttga      1046
Lys Ile Ser Leu Phe Leu Lys Asp Asp Gln
        180                 185

gtgttttggg ggatgttctt ttcttttggt gttttctgtg ttcttacaag tgtgtttatt 1106

catgcag ctt gaa tac ttg gag gag agg aga ctc aaa gac ttg gtg aag    1155
        Leu Glu Tyr Leu Glu Glu Arg Arg Leu Lys Asp Leu Val Lys
                190                 195                 200

aag cac tct gag ttc atc agt tac cct atc tac ctt tgg acc gag aaa    1203
Lys His Ser Glu Phe Ile Ser Tyr Pro Ile Tyr Leu Trp Thr Glu Lys
            205                 210                 215

acc acc gag aag gag atc agt gac gat gag gat gaa gat gaa cca aag    1251
Thr Thr Glu Lys Glu Ile Ser Asp Asp Glu Asp Glu Asp Glu Pro Lys
        220                 225                 230

aaa gaa aac gaa ggt gag gtt gaa gaa gtt gat gag aag aag gag aaa    1299
Lys Glu Asn Glu Gly Glu Val Glu Glu Val Asp Glu Lys Lys Glu Lys
    235                 240                 245

gat ggt aaa aag aag aag aaa atc aag gaa gtc tct cac gag tgg gaa    1347
Asp Gly Lys Lys Lys Lys Lys Ile Lys Glu Val Ser His Glu Trp Glu
250                 255                 260                 265

ctc atc aac aag cag aaa ccg atc tgg ttg agg aag cca gaa gag atc    1395
Leu Ile Asn Lys Gln Lys Pro Ile Trp Leu Arg Lys Pro Glu Glu Ile
                270                 275                 280

act aag gaa gag tat gct gct ttc tac aag agc ttg acc aat gac tgg    1443
Thr Lys Glu Glu Tyr Ala Ala Phe Tyr Lys Ser Leu Thr Asn Asp Trp
            285                 290                 295
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gaa gat cac tta gcc gtg aaa cac ttc tca gtg gag ggt cag cta gaa    1491
Glu Asp His Leu Ala Val Lys His Phe Ser Val Glu Gly Gln Leu Glu
        300                 305                 310

ttc aag gcc att ctc ttt gta cca aag aga gct ccg ttt gat ctc ttt    1539
Phe Lys Ala Ile Leu Phe Val Pro Lys Arg Ala Pro Phe Asp Leu Phe
    315                 320                 325

gac acg agg aag aag ttg aat aac atc aag ctt tat gtc agg agg gtg    1587
Asp Thr Arg Lys Lys Leu Asn Asn Ile Lys Leu Tyr Val Arg Arg Val
330                 335                 340                 345

ttc att atg gac aac tgt gaa gag cta atc cca gag tac ctc agc ttt    1635
Phe Ile Met Asp Asn Cys Glu Glu Leu Ile Pro Glu Tyr Leu Ser Phe
                350                 355                 360

gtg aaa ggt gtt gtt gac tct gat gac ttg cca ctc aac atc tct cgt    1683
Val Lys Gly Val Val Asp Ser Asp Asp Leu Pro Leu Asn Ile Ser Arg
            365                 370                 375

gag acg ctt caa cag aac aag atc ctt aag gtg atc agg aag aat cta    1731
Glu Thr Leu Gln Gln Asn Lys Ile Leu Lys Val Ile Arg Lys Asn Leu
        380                 385                 390

gtg aag aag tgc att gag atg ttc aac gag att gct gag aac aaa gag    1779
Val Lys Lys Cys Ile Glu Met Phe Asn Glu Ile Ala Glu Asn Lys Glu
    395                 400                 405

gac tac acc aaa ttc tat gag gct ttc tcc aag aat ctc aaa ttg ggt    1827
Asp Tyr Thr Lys Phe Tyr Glu Ala Phe Ser Lys Asn Leu Lys Leu Gly
410                 415                 420                 425

atc cat gaa gac agt cag aac agg gga aag att gct gat ctt cta cgg    1875
Ile His Glu Asp Ser Gln Asn Arg Gly Lys Ile Ala Asp Leu Leu Arg
                430                 435                 440

tac cac tcc aca aag agt ggt gat gaa atg acg agc ttc aaa gat tac    1923
Tyr His Ser Thr Lys Ser Gly Asp Glu Met Thr Ser Phe Lys Asp Tyr
            445                 450                 455

gtc aca agg atg aag gaa ggt caa aag gac att ttc tac atc act ggt    1971
Val Thr Arg Met Lys Glu Gly Gln Lys Asp Ile Phe Tyr Ile Thr Gly
        460                 465                 470

gaa agc aaa aag gcg gtg gag aat tcc ttc ttg gag agg ctg aag aag    2019
Glu Ser Lys Lys Ala Val Glu Asn Ser Phe Leu Glu Arg Leu Lys Lys
    475                 480                 485

aga ggc tac gag gta ctt tac atg gtg gat gcg att gac gaa tac gct    2067
Arg Gly Tyr Glu Val Leu Tyr Met Val Asp Ala Ile Asp Glu Tyr Ala
490                 495                 500                 505

gtt gga caa ttg aag gag tat gac ggt aag aaa ctt gtt tct gcg act    2115
Val Gly Gln Leu Lys Glu Tyr Asp Gly Lys Lys Leu Val Ser Ala Thr
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aaa gaa ggc ctc aaa ctt gaa gat gag acc gaa gaa gag aag aaa aag    2163
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Lys Glu Gly Leu Lys Leu Glu Asp Glu Thr Glu Glu Glu Lys Lys Lys
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agg gaa gag aag aag aag tcc ttc gag aat ctc tgc aag acg att aag    2211
Arg Glu Glu Lys Lys Lys Ser Phe Glu Asn Leu Cys Lys Thr Ile Lys
        540                 545                 550

gaa att ctc ggg gac aag gtt gag aag gtt gtg gtc tca gac agg att    2259
Glu Ile Leu Gly Asp Lys Val Glu Lys Val Val Val Ser Asp Arg Ile
    555                 560                 565

gtg gac tct ccc tgc tgt cta gta act ggt gaa tat gga tgg act gca    2307
Val Asp Ser Pro Cys Cys Leu Val Thr Gly Glu Tyr Gly Trp Thr Ala
570                 575                 580                 585

aat atg gag agg att atg aag gca cag gcc ttg aga gat agc agc atg    2355
Asn Met Glu Arg Ile Met Lys Ala Gln Ala Leu Arg Asp Ser Ser Met
                590                 595                 600

agt ggt tac atg tcg agc aag aaa aca atg gag atc aac ccc gac aac    2403
Ser Gly Tyr Met Ser Ser Lys Lys Thr Met Glu Ile Asn Pro Asp Asn
            605                 610                 615

ggt ata atg gag gac ctc agg aag aga gct gaa gca gac aag aat gac    2451
Gly Ile Met Glu Asp Leu Arg Lys Arg Ala Glu Ala Asp Lys Asn Asp
        620                 625                 630

aag tct gtt aaa gat ctt gtc atg ttg ctg tat gag aca gct ttg ttg    2499
Lys Ser Val Lys Asp Leu Val Met Leu Leu Tyr Glu Thr Ala Leu Leu
    635                 640                 645

acg tct gga ttt agt ctt gat gaa ccg aac act ttt gct gct agg att    2547
Thr Ser Gly Phe Ser Leu Asp Glu Pro Asn Thr Phe Ala Ala Arg Ile
650                 655                 660                 665

cac agg atg ttg aag ttg ggt ctg agt att gat gag gat gag aac gtt    2595
His Arg Met Leu Lys Leu Gly Leu Ser Ile Asp Glu Asp Glu Asn Val
                670                 675                 680

gag gaa gat ggt gat atg cct gag ttg gag gag gac gct gct gaa gag    2643
Glu Glu Asp Gly Asp Met Pro Glu Leu Glu Glu Asp Ala Ala Glu Glu
            685                 690                 695

agc aag atg gag gaa gtc gac taa gagatgaaga aattgctctt             2687
Ser Lys Met Glu Glu Val Asp
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Lys Glu Ile Phe Leu Arg Glu Leu Ile Ser Asn Ser Ser Asp Ala Leu
35 40 45

Asp Lys Ile Arg Phe Glu Ser Leu Thr Asp Lys Ser Lys Leu Asp Gly
50 55 60

Gln Pro Glu Leu Phe Ile Arg Leu Val Pro Asp Lys Pro Asn Lys Thr
65 70 75 80

Leu Ser Ile Ile Asp Ser Gly Ile Gly Met Thr Lys Ala Asp Leu Val
85 90 95

Asn Asn Leu Gly Thr Ile Ala Arg Ser Gly Thr Lys Glu Phe Met Glu
100 105 110

Ala Leu Gln Ala Gly Ala Asp Val Ser Met Ile Gly Gln Phe Gly Val
115 120 125

Gly Phe Tyr Ser Ala Tyr Leu Val Ala Glu Lys Val Val Val Thr Thr
130 135 140

Lys His Asn Asp Asp Glu Gln Tyr Val Trp Glu Ser Gln Ala Gly Gly
145 150 155 160

Ser Phe Thr Val Thr Arg Asp Val Asp Gly Glu Pro Leu Gly Arg Gly
165 170 175

Thr Lys Ile Ser Leu Phe Leu Lys Asp Asp Gln Leu Glu Tyr Leu Glu
180 185 190

Glu Arg Arg Leu Lys Asp Leu Val Lys Lys His Ser Glu Phe Ile Ser
195 200 205

Tyr Pro Ile Tyr Leu Trp Thr Glu Lys Thr Thr Glu Lys Glu Ile Ser
210 215 220

Asp Asp Glu Asp Glu Asp Glu Pro Lys Lys Glu Asn Glu Gly Glu Val
225 230 235 240

Glu Glu Val Asp Glu Lys Lys Glu Lys Asp Gly Lys Lys Lys Lys Lys
245 250 255

Ile Lys Glu Val Ser His Glu Trp Glu Leu Ile Asn Lys Gln Lys Pro
260 265 270

Ile Trp Leu Arg Lys Pro Glu Glu Ile Thr Lys Glu Glu Tyr Ala Ala
275 280 285

Phe Tyr Lys Ser Leu Thr Asn Asp Trp Glu Asp His Leu Ala Val Lys
290 295 300

His Phe Ser Val Glu Gly Gln Leu Glu Phe Lys Ala Ile Leu Phe Val
305 310 315 320

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Pro Lys Arg Ala Pro Phe Asp Leu Phe Asp Thr Arg Lys Lys Leu Asn
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Asn Ile Lys Leu Tyr Val Arg Arg Val Phe Ile Met Asp Asn Cys Glu
            340                 345                 350

Glu Leu Ile Pro Glu Tyr Leu Ser Phe Val Lys Gly Val Val Asp Ser
        355                 360                 365

Asp Asp Leu Pro Leu Asn Ile Ser Arg Glu Thr Leu Gln Gln Asn Lys
    370                 375                 380

Ile Leu Lys Val Ile Arg Lys Asn Leu Val Lys Lys Cys Ile Glu Met
385                 390                 395                 400

Phe Asn Glu Ile Ala Glu Asn Lys Glu Asp Tyr Thr Lys Phe Tyr Glu
                405                 410                 415

Ala Phe Ser Lys Asn Leu Lys Leu Gly Ile His Glu Asp Ser Gln Asn
            420                 425                 430

Arg Gly Lys Ile Ala Asp Leu Leu Arg Tyr His Ser Thr Lys Ser Gly
        435                 440                 445

Asp Glu Met Thr Ser Phe Lys Asp Tyr Val Thr Arg Met Lys Glu Gly
    450                 455                 460

Gln Lys Asp Ile Phe Tyr Ile Thr Gly Glu Ser Lys Lys Ala Val Glu
465                 470                 475                 480

Asn Ser Phe Leu Glu Arg Leu Lys Lys Arg Gly Tyr Glu Val Leu Tyr
                485                 490                 495

Met Val Asp Ala Ile Asp Glu Tyr Ala Val Gly Gln Leu Lys Glu Tyr
            500                 505                 510

Asp Gly Lys Lys Leu Val Ser Ala Thr Lys Glu Gly Leu Lys Leu Glu
        515                 520                 525

Asp Glu Thr Glu Glu Glu Lys Lys Lys Arg Glu Glu Lys Lys Lys Ser
    530                 535                 540

Phe Glu Asn Leu Cys Lys Thr Ile Lys Glu Ile Leu Gly Asp Lys Val
545                 550                 555                 560

Glu Lys Val Val Val Ser Asp Arg Ile Val Asp Ser Pro Cys Cys Leu
                565                 570                 575

Val Thr Gly Glu Tyr Gly Trp Thr Ala Asn Met Glu Arg Ile Met Lys
            580                 585                 590

Ala Gln Ala Leu Arg Asp Ser Ser Met Ser Gly Tyr Met Ser Ser Lys
        595                 600                 605

Lys Thr Met Glu Ile Asn Pro Asp Asn Gly Ile Met Glu Asp Leu Arg
    610                 615                 620
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Lys Arg Ala Glu Ala Asp Lys Asn Asp Lys Ser Val Lys Asp Leu Val
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Met Leu Leu Tyr Glu Thr Ala Leu Leu Thr Ser Gly Phe Ser Leu Asp
645 650 655

Glu Pro Asn Thr Phe Ala Ala Arg Ile His Arg Met Leu Lys Leu Gly
660 665 670

Leu Ser Ile Asp Glu Asp Glu Asn Val Glu Glu Asp Gly Asp Met Pro
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Ile Asp Ala Gln Leu Arg Gln Leu Val Pro Ala Lys Val Ser Glu Asp
15 20 25

gat aag ctt gtt gag tac gat gct ctt ctc ctt gat cgc ttt ctc gac 146
Asp Lys Leu Val Glu Tyr Asp Ala Leu Leu Leu Asp Arg Phe Leu Asp
30 35 40

att ctc cag gat tta cac ggc gag gat ctc cgt gaa acg gtt caa gag 194
Ile Leu Gln Asp Leu His Gly Glu Asp Leu Arg Glu Thr Val Gln Glu
45 50 55

tta tac gag ctt tct gct gag tat gaa ggg aag cgt gag cct agc aag 242
Leu Tyr Glu Leu Ser Ala Glu Tyr Glu Gly Lys Arg Glu Pro Ser Lys
60 65 70 75

ctt gag gag cta ggg agt gtc cta acg agt ttg gat cct ggt gac tca 290
Leu Glu Glu Leu Gly Ser Val Leu Thr Ser Leu Asp Pro Gly Asp Ser
80 85 90

att gtt atc tcc aag gct ttc tct cac atg ctt aac tta gcc aat ttg 338
Ile Val Ile Ser Lys Ala Phe Ser His Met Leu Asn Leu Ala Asn Leu
95 100 105

gct gag gag gtg cag att gct cac cgt cgc agg atc aag aag ctg aag 386
Ala Glu Glu Val Gln Ile Ala His Arg Arg Arg Ile Lys Lys Leu Lys

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        110                 115                 120

aaa ggt gat ttc gtt gat gag agt tct gca act act gaa tcc gat att    434
Lys Gly Asp Phe Val Asp Glu Ser Ser Ala Thr Thr Glu Ser Asp Ile
    125                 130                 135

gaa gag act ttt aag agg ctc gtt tcg gat ctt ggt aag tct cct gaa    482
Glu Glu Thr Phe Lys Arg Leu Val Ser Asp Leu Gly Lys Ser Pro Glu
140                 145                 150                 155

gag atc ttt gat gcc ttg aag aat cag act gtg gat ctg gtt ttg act    530
Glu Ile Phe Asp Ala Leu Lys Asn Gln Thr Val Asp Leu Val Leu Thr
                160                 165                 170

gct cat cct act cag tct gtg cgt aga tca ttg ctt cag aag cat ggg    578
Ala His Pro Thr Gln Ser Val Arg Arg Ser Leu Leu Gln Lys His Gly
            175                 180                 185

agg ata agg gac tgt ctt gct caa ctc tat gca aag gac att act cct    626
Arg Ile Arg Asp Cys Leu Ala Gln Leu Tyr Ala Lys Asp Ile Thr Pro
        190                 195                 200

gat gac aag cag gag cta gat gag tct ctg caa aga gag att caa gct    674
Asp Asp Lys Gln Glu Leu Asp Glu Ser Leu Gln Arg Glu Ile Gln Ala
    205                 210                 215

gca ttc cga aca gat gag att aga aga aca cct cca acc cca caa gat    722
Ala Phe Arg Thr Asp Glu Ile Arg Arg Thr Pro Pro Thr Pro Gln Asp
220                 225                 230                 235

gaa atg aga gct gga atg agt tat ttc cac gag aca atc tgg aaa ggt    770
Glu Met Arg Ala Gly Met Ser Tyr Phe His Glu Thr Ile Trp Lys Gly
                240                 245                 250

gtc ccc aag ttc ttg cgc cgt gtg gac aca gct ctg aaa aac att ggg    818
Val Pro Lys Phe Leu Arg Arg Val Asp Thr Ala Leu Lys Asn Ile Gly
            255                 260                 265

att gat gaa cgt gtt cct tac aat gcc cca ttg att caa ttc tct tcg    866
Ile Asp Glu Arg Val Pro Tyr Asn Ala Pro Leu Ile Gln Phe Ser Ser
        270                 275                 280

tgg atg ggc ggt gat cgt gat ggt aat ccg agg gtc aca cct gag gtc    914
Trp Met Gly Gly Asp Arg Asp Gly Asn Pro Arg Val Thr Pro Glu Val
    285                 290                 295

act aga gat gtg tgc ttg ttg gct aga atg atg gct gcc aat ctc tac    962
Thr Arg Asp Val Cys Leu Leu Ala Arg Met Met Ala Ala Asn Leu Tyr
300                 305                 310                 315

tat aac caa atc gag aat ctg atg ttt gag tta tct atg tgg cgt tgc   1010
Tyr Asn Gln Ile Glu Asn Leu Met Phe Glu Leu Ser Met Trp Arg Cys
                320                 325                 330

act gat gaa ttc cgt gtg cgg gcg gat gaa ctg cac agg aac tca agg   1058
Thr Asp Glu Phe Arg Val Arg Ala Asp Glu Leu His Arg Asn Ser Arg
            335                 340                 345
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350 355 360

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Thr Glu Pro Tyr Arg Val Ile Leu Gly Asp Val Arg Asp Lys Leu Tyr
365 370 375

cac aca cgt gag cgt tcc cgc caa ttg ctg agt aat gga atc tcg gat 1202
His Thr Arg Glu Arg Ser Arg Gln Leu Leu Ser Asn Gly Ile Ser Asp
380 385 390 395

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Ile Pro Glu Glu Ala Thr Phe Thr Asn Val Glu Gln Phe Leu Glu Pro
400 405 410

ctt gag ctc tgt tac cga tca cta tgt tca tgt ggt gac agc ccg ata 1298
Leu Glu Leu Cys Tyr Arg Ser Leu Cys Ser Cys Gly Asp Ser Pro Ile
415 420 425

gct gat gga agc ctt ctt gat ttc ttg agg caa gtc tct acc ttt gga 1346
Ala Asp Gly Ser Leu Leu Asp Phe Leu Arg Gln Val Ser Thr Phe Gly
430 435 440

ctc tcc ctt gtg aga ctt gac atc agg caa gag tct gaa cgc cac aca 1394
Leu Ser Leu Val Arg Leu Asp Ile Arg Gln Glu Ser Glu Arg His Thr
445 450 455

gat gtc ttg gat gct atc acc aag cac ttg gac atc ggt tcc tcc tat 1442
Asp Val Leu Asp Ala Ile Thr Lys His Leu Asp Ile Gly Ser Ser Tyr
460 465 470 475

aga gac tgg tct gaa gaa ggc cga cag gaa tgg ctt ctt gct gaa cta 1490
Arg Asp Trp Ser Glu Glu Gly Arg Gln Glu Trp Leu Leu Ala Glu Leu
480 485 490

agc ggc aaa cgt cca ctt ttc gga cct gat ctt ccc aaa acc gaa gaa 1538
Ser Gly Lys Arg Pro Leu Phe Gly Pro Asp Leu Pro Lys Thr Glu Glu
495 500 505

att tct gat gtc ctg gac aca ttc aaa gtc ata tct gag ctg cct tca 1586
Ile Ser Asp Val Leu Asp Thr Phe Lys Val Ile Ser Glu Leu Pro Ser
510 515 520

gat tgt ttt gga gct tat att atc tct atg gca act tca cct agt gat 1634
Asp Cys Phe Gly Ala Tyr Ile Ile Ser Met Ala Thr Ser Pro Ser Asp
525 530 535

gtg ctt gcg gtt gag ctt tta cag cgc gaa tgc cat gtg aaa aat cca 1682
Val Leu Ala Val Glu Leu Leu Gln Arg Glu Cys His Val Lys Asn Pro
540 545 550 555

ctt aga gtt gtt cca ctc ttt gag aag cta gct gat ctt gaa gca gct 1730
Leu Arg Val Val Pro Leu Phe Glu Lys Leu Ala Asp Leu Glu Ala Ala
560 565 570

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cct gcc gct gtt gca aga ctc ttt tct ata gac tgg tac aaa aac cgt   1778
Pro Ala Ala Val Ala Arg Leu Phe Ser Ile Asp Trp Tyr Lys Asn Arg
                575                 580                 585

att aac ggt aaa caa gag gtt atg att ggt tac tca gat tca ggg aaa   1826
Ile Asn Gly Lys Gln Glu Val Met Ile Gly Tyr Ser Asp Ser Gly Lys
            590                 595                 600

gat gca ggg cgt ctc tca gct gct tgg gag cta tac aaa gct caa gaa   1874
Asp Ala Gly Arg Leu Ser Ala Ala Trp Glu Leu Tyr Lys Ala Gln Glu
    605                 610                 615

gag ctt gtg aag gtt gct aag aaa tat gga gtg aag cta act atg ttc   1922
Glu Leu Val Lys Val Ala Lys Lys Tyr Gly Val Lys Leu Thr Met Phe
620                 625                 630                 635

cat ggc cgt ggt ggc aca gtc gga aga gga ggt ggt cct act cat ctt   1970
His Gly Arg Gly Gly Thr Val Gly Arg Gly Gly Gly Pro Thr His Leu
                640                 645                 650

gct ata ttg tct cag cca cca gat aca gtt aat ggc tct ctt cga gtc   2018
Ala Ile Leu Ser Gln Pro Pro Asp Thr Val Asn Gly Ser Leu Arg Val
                655                 660                 665

acg gtt cag ggt gaa gtc att gag caa tca ttt ggg gag gca cac tta   2066
Thr Val Gln Gly Glu Val Ile Glu Gln Ser Phe Gly Glu Ala His Leu
            670                 675                 680

tgc ttt aga aca ctt caa cgt ttc aca gca gct act cta gag cac gga   2114
Cys Phe Arg Thr Leu Gln Arg Phe Thr Ala Ala Thr Leu Glu His Gly
    685                 690                 695

atg aac cct ccg att tca cca aaa ccc gag tgg cgt gct ttg ctt gat   2162
Met Asn Pro Pro Ile Ser Pro Lys Pro Glu Trp Arg Ala Leu Leu Asp
700                 705                 710                 715

gaa atg gcg gtt gtt gca act gag gaa tac cga tct gtc gtt ttc caa   2210
Glu Met Ala Val Val Ala Thr Glu Glu Tyr Arg Ser Val Val Phe Gln
                720                 725                 730

gaa cct cga ttc gtc gag tat ttc cgc ctc gct act ccg gag ctg gag   2258
Glu Pro Arg Phe Val Glu Tyr Phe Arg Leu Ala Thr Pro Glu Leu Glu
                735                 740                 745

tat gga cgt atg aat att gga agt aga cct tca aag cga aaa cca agc   2306
Tyr Gly Arg Met Asn Ile Gly Ser Arg Pro Ser Lys Arg Lys Pro Ser
            750                 755                 760

ggt ggg atc gaa tct ctc cgt gca atc cca tgg atc ttt gct tgg acg   2354
Gly Gly Ile Glu Ser Leu Arg Ala Ile Pro Trp Ile Phe Ala Trp Thr
    765                 770                 775

caa aca aga ttc cat ctt cct gta tgg tta ggt ttc gga gca gca ttt   2402
Gln Thr Arg Phe His Leu Pro Val Trp Leu Gly Phe Gly Ala Ala Phe
780                 785                 790                 795

agg tat gcg atc aag aag gat gtg aga aac ctt cac atg ctg caa gat   2450
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Arg Tyr Ala Ile Lys Lys Asp Val Arg Asn Leu His Met Leu Gln Asp
800 805 810

atg tat aaa caa tgg ccc ttt ttc cga gtc acc atc gat cta att gaa 2498
Met Tyr Lys Gln Trp Pro Phe Phe Arg Val Thr Ile Asp Leu Ile Glu
815 820 825

atg gtg ttc gcc aag gga gac ccc ggg atc gct gct ttg tac gac aaa 2546
Met Val Phe Ala Lys Gly Asp Pro Gly Ile Ala Ala Leu Tyr Asp Lys
830 835 840

ctt ctt gtc tca gaa gat tta tgg gct ttt gga gag aaa ctc aga gcc 2594
Leu Leu Val Ser Glu Asp Leu Trp Ala Phe Gly Glu Lys Leu Arg Ala
845 850 855

aac ttt gat gaa acc aag aac ctc gtc ctc cag act gct gga cat aaa 2642
Asn Phe Asp Glu Thr Lys Asn Leu Val Leu Gln Thr Ala Gly His Lys
860 865 870 875

gac ctt ctt gaa gga gat cct tac ttg aaa cag aga cta agg cta cgt 2690
Asp Leu Leu Glu Gly Asp Pro Tyr Leu Lys Gln Arg Leu Arg Leu Arg
880 885 890

gac tct tac att acg acc ctc aac gtt tgc caa gcc tac aca ttg aag 2738
Asp Ser Tyr Ile Thr Thr Leu Asn Val Cys Gln Ala Tyr Thr Leu Lys
895 900 905

agg atc cgt gat gca aac tac aat gtg act ctg cga cca cac att tct 2786
Arg Ile Arg Asp Ala Asn Tyr Asn Val Thr Leu Arg Pro His Ile Ser
910 915 920

aaa gag atc atg caa tca agc aaa tca gca caa gag ctc gtc aag ctt 2834
Lys Glu Ile Met Gln Ser Ser Lys Ser Ala Gln Glu Leu Val Lys Leu
925 930 935

aac ccc acg agt gaa tac gcg cct gga ctt gag gac aca ctt atc tta 2882
Asn Pro Thr Ser Glu Tyr Ala Pro Gly Leu Glu Asp Thr Leu Ile Leu
940 945 950 955

acc atg aag ggt att gct gca gga ttg caa aac acc ggt taa gtgagtca 2932
Thr Met Lys Gly Ile Ala Ala Gly Leu Gln Asn Thr Gly
960 965

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<211> 968
<212> PRT
<213> Arabidopsis thaliana

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Met Ala Gly Arg Asn Ile Glu Lys Met Ala Ser Ile Asp Ala Gln Leu
1 5 10 15

Arg Gln Leu Val Pro Ala Lys Val Ser Glu Asp Asp Lys Leu Val Glu
20 25 30

Tyr Asp Ala Leu Leu Leu Asp Arg Phe Leu Asp Ile Leu Gln Asp Leu

35 40 45

His Gly Glu Asp Leu Arg Glu Thr Val Gln Glu Leu Tyr Glu Leu Ser
50 55 60

Ala Glu Tyr Glu Gly Lys Arg Glu Pro Ser Lys Leu Glu Glu Leu Gly
65 70 75 80

Ser Val Leu Thr Ser Leu Asp Pro Gly Asp Ser Ile Val Ile Ser Lys
85 90 95

Ala Phe Ser His Met Leu Asn Leu Ala Asn Leu Ala Glu Glu Val Gln
100 105 110

Ile Ala His Arg Arg Arg Ile Lys Lys Leu Lys Lys Gly Asp Phe Val
115 120 125

Asp Glu Ser Ser Ala Thr Thr Glu Ser Asp Ile Glu Glu Thr Phe Lys
130 135 140

Arg Leu Val Ser Asp Leu Gly Lys Ser Pro Glu Glu Ile Phe Asp Ala
145 150 155 160

Leu Lys Asn Gln Thr Val Asp Leu Val Leu Thr Ala His Pro Thr Gln
165 170 175

Ser Val Arg Arg Ser Leu Leu Gln Lys His Gly Arg Ile Arg Asp Cys
180 185 190

Leu Ala Gln Leu Tyr Ala Lys Asp Ile Thr Pro Asp Asp Lys Gln Glu
195 200 205

Leu Asp Glu Ser Leu Gln Arg Glu Ile Gln Ala Ala Phe Arg Thr Asp
210 215 220

Glu Ile Arg Arg Thr Pro Pro Thr Pro Gln Asp Glu Met Arg Ala Gly
225 230 235 240

Met Ser Tyr Phe His Glu Thr Ile Trp Lys Gly Val Pro Lys Phe Leu
245 250 255

Arg Arg Val Asp Thr Ala Leu Lys Asn Ile Gly Ile Asp Glu Arg Val
260 265 270

Pro Tyr Asn Ala Pro Leu Ile Gln Phe Ser Ser Trp Met Gly Gly Asp
275 280 285

Arg Asp Gly Asn Pro Arg Val Thr Pro Glu Val Thr Arg Asp Val Cys
290 295 300

Leu Leu Ala Arg Met Met Ala Ala Asn Leu Tyr Tyr Asn Gln Ile Glu
305 310 315 320

Asn Leu Met Phe Glu Leu Ser Met Trp Arg Cys Thr Asp Glu Phe Arg
325 330 335

Val Arg Ala Asp Glu Leu His Arg Asn Ser Arg Lys Asp Ala Ala Lys

340 345 350

His Tyr Ile Glu Phe Trp Lys Thr Ile Pro Pro Thr Glu Pro Tyr Arg
355 360 365

Val Ile Leu Gly Asp Val Arg Asp Lys Leu Tyr His Thr Arg Glu Arg
370 375 380

Ser Arg Gln Leu Leu Ser Asn Gly Ile Ser Asp Ile Pro Glu Glu Ala
385 390 395 400

Thr Phe Thr Asn Val Glu Gln Phe Leu Glu Pro Leu Glu Leu Cys Tyr
405 410 415

Arg Ser Leu Cys Ser Cys Gly Asp Ser Pro Ile Ala Asp Gly Ser Leu
420 425 430

Leu Asp Phe Leu Arg Gln Val Ser Thr Phe Gly Leu Ser Leu Val Arg
435 440 445

Leu Asp Ile Arg Gln Glu Ser Glu Arg His Thr Asp Val Leu Asp Ala
450 455 460

Ile Thr Lys His Leu Asp Ile Gly Ser Ser Tyr Arg Asp Trp Ser Glu
465 470 475 480

Glu Gly Arg Gln Glu Trp Leu Leu Ala Glu Leu Ser Gly Lys Arg Pro
485 490 495

Leu Phe Gly Pro Asp Leu Pro Lys Thr Glu Glu Ile Ser Asp Val Leu
500 505 510

Asp Thr Phe Lys Val Ile Ser Glu Leu Pro Ser Asp Cys Phe Gly Ala
515 520 525

Tyr Ile Ile Ser Met Ala Thr Ser Pro Ser Asp Val Leu Ala Val Glu
530 535 540

Leu Leu Gln Arg Glu Cys His Val Lys Asn Pro Leu Arg Val Val Pro
545 550 555 560

Leu Phe Glu Lys Leu Ala Asp Leu Glu Ala Ala Pro Ala Ala Val Ala
565 570 575

Arg Leu Phe Ser Ile Asp Trp Tyr Lys Asn Arg Ile Asn Gly Lys Gln
580 585 590

Glu Val Met Ile Gly Tyr Ser Asp Ser Gly Lys Asp Ala Gly Arg Leu
595 600 605

Ser Ala Ala Trp Glu Leu Tyr Lys Ala Gln Glu Glu Leu Val Lys Val
610 615 620

Ala Lys Lys Tyr Gly Val Lys Leu Thr Met Phe His Gly Arg Gly Gly
625 630 635 640

Thr Val Gly Arg Gly Gly Gly Pro Thr His Leu Ala Ile Leu Ser Gln

645 650 655

Pro Pro Asp Thr Val Asn Gly Ser Leu Arg Val Thr Val Gln Gly Glu
660 665 670

Val Ile Glu Gln Ser Phe Gly Glu Ala His Leu Cys Phe Arg Thr Leu
675 680 685

Gln Arg Phe Thr Ala Ala Thr Leu Glu His Gly Met Asn Pro Pro Ile
690 695 700

Ser Pro Lys Pro Glu Trp Arg Ala Leu Leu Asp Glu Met Ala Val Val
705 710 715 720

Ala Thr Glu Glu Tyr Arg Ser Val Val Phe Gln Glu Pro Arg Phe Val
725 730 735

Glu Tyr Phe Arg Leu Ala Thr Pro Glu Leu Glu Tyr Gly Arg Met Asn
740 745 750

Ile Gly Ser Arg Pro Ser Lys Arg Lys Pro Ser Gly Gly Ile Glu Ser
755 760 765

Leu Arg Ala Ile Pro Trp Ile Phe Ala Trp Thr Gln Thr Arg Phe His
770 775 780

Leu Pro Val Trp Leu Gly Phe Gly Ala Ala Phe Arg Tyr Ala Ile Lys
785 790 795 800

Lys Asp Val Arg Asn Leu His Met Leu Gln Asp Met Tyr Lys Gln Trp
805 810 815

Pro Phe Phe Arg Val Thr Ile Asp Leu Ile Glu Met Val Phe Ala Lys
820 825 830

Gly Asp Pro Gly Ile Ala Ala Leu Tyr Asp Lys Leu Leu Val Ser Glu
835 840 845

Asp Leu Trp Ala Phe Gly Glu Lys Leu Arg Ala Asn Phe Asp Glu Thr
850 855 860

Lys Asn Leu Val Leu Gln Thr Ala Gly His Lys Asp Leu Leu Glu Gly
865 870 875 880

Asp Pro Tyr Leu Lys Gln Arg Leu Arg Leu Arg Asp Ser Tyr Ile Thr
885 890 895

Thr Leu Asn Val Cys Gln Ala Tyr Thr Leu Lys Arg Ile Arg Asp Ala
900 905 910

Asn Tyr Asn Val Thr Leu Arg Pro His Ile Ser Lys Glu Ile Met Gln
915 920 925

Ser Ser Lys Ser Ala Gln Glu Leu Val Lys Leu Asn Pro Thr Ser Glu
930 935 940

Tyr Ala Pro Gly Leu Glu Asp Thr Leu Ile Leu Thr Met Lys Gly Ile

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945                 950                 955                 960

Ala Ala Gly Leu Gln Asn Thr Gly
                965
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<211> 271
<212> DNA
<213> Arabidopsis thaliana

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<222> (17)..(259)

<400> 15

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                  Met Ser Arg Ala Thr Tyr Ile Ile Gly Ala Leu Ala
                    1               5                  10

gga tct gcg gta gta gct tac gtg tgt gac aaa gtt att tct gat gat  100
Gly Ser Ala Val Val Ala Tyr Val Cys Asp Lys Val Ile Ser Asp Asp
        15                  20                  25

aag ctt ttt gga ggt act aca cca gga act att act aac aag gaa tgg  148
Lys Leu Phe Gly Gly Thr Thr Pro Gly Thr Ile Thr Asn Lys Glu Trp
    30                  35                  40

ggt gct gcg act gaa gag aga tta caa gca tgg cca aga gtt gct ggt  196
Gly Ala Ala Thr Glu Glu Arg Leu Gln Ala Trp Pro Arg Val Ala Gly
45                  50                  55                  60

cct ccc gtc gtc atg aac cct atc agt cgc cag aat ttc atc gtc aag  244
Pro Pro Val Val Met Asn Pro Ile Ser Arg Gln Asn Phe Ile Val Lys
                65                  70                  75

tca cgt cct gaa taa cttttgatgc ct                                271
Ser Arg Pro Glu
            80
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<210> 16
<211> 80
<212> PRT
<213> Arabidopsis thaliana

<400> 16

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Met Ser Arg Ala Thr Tyr Ile Ile Gly Ala Leu Ala Gly Ser Ala Val
1               5                   10                  15

Val Ala Tyr Val Cys Asp Lys Val Ile Ser Asp Asp Lys Leu Phe Gly
            20                  25                  30

Gly Thr Thr Pro Gly Thr Ile Thr Asn Lys Glu Trp Gly Ala Ala Thr
        35                  40                  45
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Glu Glu Arg Leu Gln Ala Trp Pro Arg Val Ala Gly Pro Pro Val Val
     50                  55                  60

Met Asn Pro Ile Ser Arg Gln Asn Phe Ile Val Lys Ser Arg Pro Glu
 65                  70                  75                  80



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<211> 2580
<212> DNA
<213> Arabidopsis thaliana

<220>
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<222> (30)..(143)

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<222> (1334)..(1383)

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<222> (1497)..(1577)

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<222> (1882)..(1984)

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<400> 17
tcttcacaaa tcctaaacga gtaggagct atg gct gca ccg att gtt gat gcg    53
                                Met Ala Ala Pro Ile Val Asp Ala
                                 1               5

gag tac ttg aaa gag atc act aag gct cgc cgt gag ctc cgt tct ctc   101
Glu Tyr Leu Lys Glu Ile Thr Lys Ala Arg Arg Glu Leu Arg Ser Leu
     10                  15                  20
```

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atc gcg aac aag aac tgt gct cct atc atg ctc cga ttg gcg          143
Ile Ala Asn Lys Asn Cys Ala Pro Ile Met Leu Arg Leu Ala
 25                 30                  35

taagttttcg atttccttgg tttttcgtcg agttgactgt tacagatttc gtttattcat 203

gtggagatcg ttcgattgta gttaggctgt agaatcgatt ttgtttgttt ttgaatgttg 263

aaatgtttgt atcatctggt ttttatgaag a tgg cac gat gct gga acc tat   315
                                   Trp His Asp Ala Gly Thr Tyr
                                       40                  45

gat gct caa tcg aag acc ggt gga cct aat ggc tct atc agg aac gaa  363
Asp Ala Gln Ser Lys Thr Gly Gly Pro Asn Gly Ser Ile Arg Asn Glu
                50                  55                  60

gaa gag cac act cat ggt gcc aac agt ggt ttg aag atc gct ctc gat  411
Glu Glu His Thr His Gly Ala Asn Ser Gly Leu Lys Ile Ala Leu Asp
            65                  70                  75

ctc tgt ggtaggattt tgatttagtt tttgtagatt cactttctgg ataatttcat   467
Leu Cys

gcgatgtatc cgttttatgt tgtggtttaa gaacactgtt caaaataatt acattatgct 527

tttggaaatg gactttgtat cgcttaatta tgagatccta tctttgatgt ttca gag   584
                                                            Glu
                                                             80

ggc gtg aaa gct aag cat ccc aaa atc aca tac gca gac ctg tat cag  632
Gly Val Lys Ala Lys His Pro Lys Ile Thr Tyr Ala Asp Leu Tyr Gln
                85                  90                  95

gtgagttaag gctgtgagag aaatcttttt gatgtccttg ttgctttttc tgcacatttg 692

tttttcaaag ttcgctggaa ctgtattcgg cttgtgtcat tacctcgtcc caggtttgag 752

cttgttgttt aggagactta gttgatagtt gagcagctgt gtaaatatgg tttcagttgt 812

aatttgtttc aggagatgtt actgattgtg atttggttta caaaaatcat agattgacta 872

tgttgttcaa ctagaacttt tatctcttgc agtaatagct aaattcaagt aaaatataca 932

ctgaatgaat tcaaacgacc aagaaggaaa ctgtaatgta atgtcaatct gtttccatcc 992

taagtcacat gtctgtcgtc tgtacctata acctgtctct acgactgttt gtattgccgt 1052

ttctccattt tatatttggt cttacaaggt cgaggcttta tttatgaatt cccaatagaa 1112

gtgtaccagt ttaatggcaa ttaagttttg ggtatgaatt atttactttt aagtgttttg 1172

tttcag ctt gct ggt gtg gta gca gtt gag gtt act ggt gga cct gac   1220
       Leu Ala Gly Val Val Ala Val Glu Val Thr Gly Gly Pro Asp
                  100                 105                 110

atc gtg ttc gtt ccc ggg aga aag g tatactttct catctcttga          1265
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Ile Val Phe Val Pro Gly Arg Lys A
                115

gacattataa cagcttatca gtttaacact aaagcaaaca taattactgt atgtttcttc 1325

ttgatagg at tca aat gtc tgc ccc aag gaa gga aga ctt cct gat gcc  1374
         sp Ser Asn Val Cys Pro Lys Glu Gly Arg Leu Pro Asp Ala
            120                 125                 130

aaa caa ggt acactaaatt cttgtatcaa ttataacaaa cttttcatgt         1423
Lys Gln Gly
        135

tttctactga taatcttgtt ttggaattgg aagatttttt ctatgaattc acattgttta 1483

tatctctgta ggt ttc caa cat ctc aga gat gtc ttc tac cgc atg gga   1532
               Phe Gln His Leu Arg Asp Val Phe Tyr Arg Met Gly
                               140                 145

cta tct gat aag gat att gtg gca ctc tca ggg ggt cat act ctg      1577
Leu Ser Asp Lys Asp Ile Val Ala Leu Ser Gly Gly His Thr Leu
        150                 155                 160

gtaaattcat tggtcactta cttaacttcc gttgtttttg aacaaatatg cttgttgtgc 1637

ttatgaccac attgggtgtt tag gga agg gct cac ccg gag agg tca ggc ttt 1690
                          Gly Arg Ala His Pro Glu Arg Ser Gly Phe
                                  165                 170

gat gga cca tgg acc caa gag ccg ctg aat ttt gac aac tcc tac ttc  1738
Asp Gly Pro Trp Thr Gln Glu Pro Leu Asn Phe Asp Asn Ser Tyr Phe
        175                 180                 185

gt gtaattttca tttctttatc ctcagagatt ttctttgtgc attttttaa         1790
Va

tcttttctgt ttgtgtctcc aagaaataaa agcagcaaac agatactttt ttacatgatc 1850

ggttatccat gattatttac tgttttggta c c agg gaa ctg ctg aaa gga gaa  1903
                                   l Arg Glu Leu Leu Lys Gly Glu
                                     190                 195

tca gag ggc ttg ttg aaa ctt cca act gac aag acc tta ttg gaa gac  1951
Ser Glu Gly Leu Leu Lys Leu Pro Thr Asp Lys Thr Leu Leu Glu Asp
            200                 205                 210

ccg gag ttc cgt cgt ctt gtt gag ctt tat gca aaggtataat atactggaga 2004
Pro Glu Phe Arg Arg Leu Val Glu Leu Tyr Ala
        215                 220

tcttctctgc ctctttgcca tttgtttctt gcgttgctat aataaccatt ggaacataac 2064

tcgatttcct ttattggttt cacattttca ctgaatccac aagcacacac actgaatcac 2124

aaaccaaatt atctagggtt ttgttctaga gaaccccacg gatccttatc gcctttatag 2184

ttgctgatgt tgcaaaatga taaaatgaac actcttacta ctatcagtga gaactgtaat 2244
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attagctttt tgttagaacc gtaaacagaa attcctatgg ttctttatga tttccttgct 2304

taattaagtt tcaataagat aagaaagtgt tgttatgtgt tgacaagttc agtttgtggt 2364

ggcag gat gaa gat gca ttc ttc aga gac tac gcg gaa tcg cac aag aaa 2414
      Asp Glu Asp Ala Phe Phe Arg Asp Tyr Ala Glu Ser His Lys Lys
          225                 230                 235

ctc tct gag ctt ggt ttc aac cca aac tcc tca gca ggc aaa gca gtt   2462
Leu Ser Glu Leu Gly Phe Asn Pro Asn Ser Ser Ala Gly Lys Ala Val
    240                 245                 250

gca gac agc acg att ctg gca cag agt gcg ttc ggg gtt gca gtt gct   2510
Ala Asp Ser Thr Ile Leu Ala Gln Ser Ala Phe Gly Val Ala Val Ala
255                 260                 265                 270

gct gcg gtt gtg gca ttt ggt tac ttt tac gag atc cgg aag agg atg   2558
Ala Ala Val Val Ala Phe Gly Tyr Phe Tyr Glu Ile Arg Lys Arg Met
                275                 280                 285

aag taa acgaaatagg aagtaa                                         2580
Lys
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<210> 18
<211> 287
<212> PRT
<213> Arabidopsis thaliana

<400> 18

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  1               5                  10                  15

Ala Arg Arg Glu Leu Arg Ser Leu Ile Ala Asn Lys Asn Cys Ala Pro
             20                  25                  30

Ile Met Leu Arg Leu Ala Trp His Asp Ala Gly Thr Tyr Asp Ala Gln
         35                  40                  45

Ser Lys Thr Gly Gly Pro Asn Gly Ser Ile Arg Asn Glu Glu Glu His
     50                  55                  60

Thr His Gly Ala Asn Ser Gly Leu Lys Ile Ala Leu Asp Leu Cys Glu
 65                  70                  75                  80

Gly Val Lys Ala Lys His Pro Lys Ile Thr Tyr Ala Asp Leu Tyr Gln
                 85                  90                  95

Leu Ala Gly Val Val Ala Val Glu Val Thr Gly Gly Pro Asp Ile Val
            100                 105                 110

Phe Val Pro Gly Arg Lys Asp Ser Asn Val Cys Pro Lys Glu Gly Arg
        115                 120                 125

Leu Pro Asp Ala Lys Gln Gly Phe Gln His Leu Arg Asp Val Phe Tyr
    130                 135                 140
```

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Arg Met Gly Leu Ser Asp Lys Asp Ile Val Ala Leu Ser Gly Gly His
145                 150                 155                 160

Thr Leu Gly Arg Ala His Pro Glu Arg Ser Gly Phe Asp Gly Pro Trp
                165                 170                 175

Thr Gln Glu Pro Leu Asn Phe Asp Asn Ser Tyr Phe Val Arg Glu Leu
            180                 185                 190

Leu Lys Gly Glu Ser Glu Gly Leu Leu Lys Leu Pro Thr Asp Lys Thr
        195                 200                 205

Leu Leu Glu Asp Pro Glu Phe Arg Arg Leu Val Glu Leu Tyr Ala Asp
    210                 215                 220

Glu Asp Ala Phe Phe Arg Asp Tyr Ala Glu Ser His Lys Lys Leu Ser
225                 230                 235                 240

Glu Leu Gly Phe Asn Pro Asn Ser Ser Ala Gly Lys Ala Val Ala Asp
                245                 250                 255

Ser Thr Ile Leu Ala Gln Ser Ala Phe Gly Val Ala Val Ala Ala Ala
            260                 265                 270

Val Val Ala Phe Gly Tyr Phe Tyr Glu Ile Arg Lys Arg Met Lys
        275                 280                 285


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<211> 1861
<212> DNA
<213> Arabidopsis thaliana

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<222> (26)..(284)

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<221> CDS
<222> (541)..(917)

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<222> (1257)..(1493)

<220>
<221> CDS
<222> (1584)..(1853)

<400> 19
atagaaaaac cctaagtagg ttgtg atg ttg cga gct tta gca cgg cct ctc    52
                            Met Leu Arg Ala Leu Ala Arg Pro Leu
                            1               5

gaa cgg tgt ttg gga agc aga gct agt ggt gat ggt tta ctc tgg caa    100
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Glu Arg Cys Leu Gly Ser Arg Ala Ser Gly Asp Gly Leu Leu Trp Gln
 10                 15                  20                  25

tcg gaa ttg aga cct cac gct ggc ggt gat tat tcg atc gcg gtg gtt    148
Ser Glu Leu Arg Pro His Ala Gly Gly Asp Tyr Ser Ile Ala Val Val
                30                  35                  40

caa gcc aat tcc agg ctt gaa gat cag agt cag gtt ttc aca tct tct    196
Gln Ala Asn Ser Arg Leu Glu Asp Gln Ser Gln Val Phe Thr Ser Ser
            45                  50                  55

tct gct act tac gtc ggt gta tac gat ggt cat ggt gga cct gaa gct    244
Ser Ala Thr Tyr Val Gly Val Tyr Asp Gly His Gly Gly Pro Glu Ala
        60                  65                  70

tct aga ttc gtt aac aga cat ctc ttt cct tat atg cac a gtaagttata   294
Ser Arg Phe Val Asn Arg His Leu Phe Pro Tyr Met His L
    75                  80                  85

atcccactct tccttcccta aacttgtttt aggattcttt cttcttttga ctctttgact 354

acgtttttga tggtcaaaac ttatgagatc tctattaccc tgatcatttc aatattaaaa 414

gattcgaatt ttgctatgaa gttttggtct ttgtgaacat gttcaggttt gtaaattgcc 474

tcttgaattg attttgtagt catgttcttg ttagtgaaat ttacaggatt ggttttatga 534

ttgcag aa ttt gca aga gaa cat ggg gga tta tct gta gat gtt atc aaa 584
       ys Phe Ala Arg Glu His Gly Gly Leu Ser Val Asp Val Ile Lys
                    90                  95                  100

aag gca ttc aaa gaa aca gaa gaa gag ttt tgt ggt atg gtt aaa cga    632
Lys Ala Phe Lys Glu Thr Glu Glu Glu Phe Cys Gly Met Val Lys Arg
            105                 110                 115

tcc ctt ccc atg aaa ccg caa atg gct act gta gga tct tgc tgt ctt    680
Ser Leu Pro Met Lys Pro Gln Met Ala Thr Val Gly Ser Cys Cys Leu
        120                 125                 130

gtt ggt gca atc tct aat gac aca ctg tat gtt gct aat ctt ggg gac    728
Val Gly Ala Ile Ser Asn Asp Thr Leu Tyr Val Ala Asn Leu Gly Asp
    135                 140                 145

tcg aga gcc gtt ctt gga agc gtt gtt tca ggg gtt gat agt aat aaa    776
Ser Arg Ala Val Leu Gly Ser Val Val Ser Gly Val Asp Ser Asn Lys
150                 155                 160                 165

ggt gcc gta gct gaa cgg tta tct act gat cat aat gtt gct gtt gaa    824
Gly Ala Val Ala Glu Arg Leu Ser Thr Asp His Asn Val Ala Val Glu
                170                 175                 180

gaa gtg aga aag gag gtt aag gca ctt aac cct gat gac tca caa atc    872
Glu Val Arg Lys Glu Val Lys Ala Leu Asn Pro Asp Asp Ser Gln Ile
            185                 190                 195

gtc tta tac aca cgt gga gtt tgg cgg att aaa ggc att att cag        917
Val Leu Tyr Thr Arg Gly Val Trp Arg Ile Lys Gly Ile Ile Gln
```

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        200                 205                 210

gtataactta gttttgcttg cctgcttgtt aaattgcgtg tgattacata gcatctgtga 977

tgaagttata atatttaaaa ggtgtaatct gatgttgttt tttcttttct cttttcattt 1037

atataaatgg gggcttgcaa tgttccagga atccgtcaca cgggctcctg caacgtttct 1097

tccccagtgg attttgtgct tttctaagaa ttcccggtag tcagagctat acataataat 1157

gaagatacat gctttttagt tgcttgtgac ctttccgtga atgtttgagc tcgttgtata 1217

ttagttagct aaatcgtttt catatacgct tctttatag gta tcg aga tca att   1271
                                          Val Ser Arg Ser Ile
                                                      215

ggg gat gta tac ttg aaa aaa ccg gag tat tac agg gac ccg att ttc   1319
Gly Asp Val Tyr Leu Lys Lys Pro Glu Tyr Tyr Arg Asp Pro Ile Phe
        220                 225                 230

cag cga cat gga aat ccc att cct ttg agg aga ccc gcg atg aca gcc   1367
Gln Arg His Gly Asn Pro Ile Pro Leu Arg Arg Pro Ala Met Thr Ala
    235                 240                 245

gaa ccc tcc att ata gta agg aag ctt aag cca cag gac ttg ttt ctg   1415
Glu Pro Ser Ile Ile Val Arg Lys Leu Lys Pro Gln Asp Leu Phe Leu
250                 255                 260                 265

ata ttt gca tca gat ggt ctc tgg gaa cat ctt agt gat gaa aca gcc   1463
Ile Phe Ala Ser Asp Gly Leu Trp Glu His Leu Ser Asp Glu Thr Ala
                270                 275                 280

gta gaa atc gtc ctc aaa cac cca aga act gtaagttttc cctaaactca     1513
Val Glu Ile Val Leu Lys His Pro Arg Thr
            285                 290

agtttgcttt gtatcttcac atttatgtta gctacttagt ttatttattt attaactctg 1573

tgttctacag ggt att gcc cga aga ctt gta aga gct gct ctg gaa gaa    1622
           Gly Ile Ala Arg Arg Leu Val Arg Ala Ala Leu Glu Glu
                       295                 300

gcg gca aag aag aga gaa atg aga tat gga gat ata aag aaa ata gcc   1670
Ala Ala Lys Lys Arg Glu Met Arg Tyr Gly Asp Ile Lys Lys Ile Ala
305                 310                 315                 320

aaa gga att cga cga cat ttc cat gac gac ata agc gtt att gta gtt   1718
Lys Gly Ile Arg Arg His Phe His Asp Asp Ile Ser Val Ile Val Val
                325                 330                 335

tat cta gat caa aac aaa acc agt tca tcg aat agt aaa ttg gtg aag   1766
Tyr Leu Asp Gln Asn Lys Thr Ser Ser Ser Asn Ser Lys Leu Val Lys
            340                 345                 350

caa gga ggt atc acc gct cca ccg gat atc tac tca tta cac tct gat   1814
Gln Gly Gly Ile Thr Ala Pro Pro Asp Ile Tyr Ser Leu His Ser Asp
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35 40 45

Asp Gln Ser Gln Val Phe Thr Ser Ser Ser Ala Thr Tyr Val Gly Val
50 55 60

Tyr Asp Gly His Gly Gly Pro Glu Ala Ser Arg Phe Val Asn Arg His
65 70 75 80

Leu Phe Pro Tyr Met His Lys Phe Ala Arg Glu His Gly Gly Leu Ser
85 90 95

Val Asp Val Ile Lys Lys Ala Phe Lys Glu Thr Glu Glu Glu Phe Cys
100 105 110

Gly Met Val Lys Arg Ser Leu Pro Met Lys Pro Gln Met Ala Thr Val
115 120 125

Gly Ser Cys Cys Leu Val Gly Ala Ile Ser Asn Asp Thr Leu Tyr Val
130 135 140

Ala Asn Leu Gly Asp Ser Arg Ala Val Leu Gly Ser Val Val Ser Gly
145 150 155 160

Val Asp Ser Asn Lys Gly Ala Val Ala Glu Arg Leu Ser Thr Asp His
165 170 175

Asn Val Ala Val Glu Glu Val Arg Lys Glu Val Lys Ala Leu Asn Pro
180 185 190

Asp Asp Ser Gln Ile Val Leu Tyr Thr Arg Gly Val Trp Arg Ile Lys
195 200 205

Gly Ile Ile Gln Val Ser Arg Ser Ile Gly Asp Val Tyr Leu Lys Lys
210 215 220

Pro Glu Tyr Tyr Arg Asp Pro Ile Phe Gln Arg His Gly Asn Pro Ile
225 230 235 240

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Pro Leu Arg Arg Pro Ala Met Thr Ala Glu Pro Ser Ile Ile Val Arg
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Lys Leu Lys Pro Gln Asp Leu Phe Leu Ile Phe Ala Ser Asp Gly Leu
            260                 265                 270

Trp Glu His Leu Ser Asp Glu Thr Ala Val Glu Ile Val Leu Lys His
        275                 280                 285

Pro Arg Thr Gly Ile Ala Arg Arg Leu Val Arg Ala Ala Leu Glu Glu
    290                 295                 300

Ala Ala Lys Lys Arg Glu Met Arg Tyr Gly Asp Ile Lys Lys Ile Ala
305                 310                 315                 320

Lys Gly Ile Arg Arg His Phe His Asp Asp Ile Ser Val Ile Val Val
                325                 330                 335

Tyr Leu Asp Gln Asn Lys Thr Ser Ser Ser Asn Ser Lys Leu Val Lys
            340                 345                 350

Gln Gly Gly Ile Thr Ala Pro Pro Asp Ile Tyr Ser Leu His Ser Asp
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Glu Ala Glu Gln Arg Arg Leu Leu Asn Val Leu Tyr
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                                            Met Thr Lys Arg Lys
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aag gaa gta ata gat gtc gat tgc tcc gag aag aaa gat ttt gtg att   103
Lys Glu Val Ile Asp Val Asp Cys Ser Glu Lys Lys Asp Phe Val Ile
                10                  15                  20

gat tgg tct tcc gct atg gat aag gaa gac gaa gtt ccc gag ctc gag   151
Asp Trp Ser Ser Ala Met Asp Lys Glu Asp Glu Val Pro Glu Leu Glu
            25                  30                  35

att gtt aat acc acc aaa cct act cct ccg cca ccg cca acg ttt ttc   199
Ile Val Asn Thr Thr Lys Pro Thr Pro Pro Pro Pro Pro Thr Phe Phe
        40                  45                  50

tcc gac gat caa acc gat tct ccg aaa ctc cta acc gat cgt gac ctc   247
Ser Asp Asp Gln Thr Asp Ser Pro Lys Leu Leu Thr Asp Arg Asp Leu
    55                  60                  65

gac gag cag cta gag cgt aaa aaa gcg atc ctg aca tta ggt ccg ggc   295
Asp Glu Gln Leu Glu Arg Lys Lys Ala Ile Leu Thr Leu Gly Pro Gly
70                  75                  80                  85

tta ccc gac aag ggt gag aaa att cga ctc aaa atc gct gat ctc gaa   343
Leu Pro Asp Lys Gly Glu Lys Ile Arg Leu Lys Ile Ala Asp Leu Glu
                90                  95                  100

gag gag aag cag c gtagagtttt agaaggctcg aaaatggttc gcattctgat     396
Glu Glu Lys Gln A
            105
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tcaattgcat gcttagttcg tttgattttc ttagatatgt tactgtttta ggttggggtt 456

ttcaagttta tgctaaagtt tggctttttt tgagtacatt tatgtgtatc tttactggtc 516

ttacctcata gtccaagcta gattcgagct catttatgtg tatgatctat agtcacagaa 576

catctatgtg ttcgagctca tttatgtgtt tgaatatgaa tatgatgcta caaaagactt 636

ttttggcagg aggtggacag aagttctaag gtcgtgtctt cgactagctc aggtattctt 696

ggtggataat gttaaagttg tttgcttcta acatagtggt tcatttttct gtatggtttt 756

tcgatttatc tttcattttt tggacttaag tttgatgagc catgtttcat gtag gt    812
                                                             rg

tca gat gtt tta ccg caa gga aat gca gtt tca aaa gat acc tct aga   860
Ser Asp Val Leu Pro Gln Gly Asn Ala Val Ser Lys Asp Thr Ser Arg
            110                 115                 120

ggg aat gca gac tca aaa gac acc tct aga caa ggg aat gca gat tca   908
Gly Asn Ala Asp Ser Lys Asp Thr Ser Arg Gln Gly Asn Ala Asp Ser
        125                 130                 135

aaa gaa gtc tca cgg tca aca ttt tct gcg gtt ttc agt aaa cca aaa   956
Lys Glu Val Ser Arg Ser Thr Phe Ser Ala Val Phe Ser Lys Pro Lys
    140                 145                 150

gtatggagca tcgttttttt tttttgttc aacgtatgga gcctctatat tttgcaattt 1016

taaaactgtt ttggatgggt acttcttcat gatacgattt tgtaatctgt gttcaacag  1075

acg gat tct cag tca aag aaa gcc ttt ggt aaa gaa cta gaa gat ctg   1123
Thr Asp Ser Gln Ser Lys Lys Ala Phe Gly Lys Glu Leu Glu Asp Leu
155                 160                 165                 170

gga tgt gaa agg agg aaa cac aag gct ggt aga aag cct gta aca agg   1171
Gly Cys Glu Arg Arg Lys His Lys Ala Gly Arg Lys Pro Val Thr Arg
                175                 180                 185

ctg agc aac ggg tgg cgg ttg ttg cca gat gta ggg aaa gct gag cac   1219
Leu Ser Asn Gly Trp Arg Leu Leu Pro Asp Val Gly Lys Ala Glu His
            190                 195                 200

agt gca aag cag ttt gat tct gga ctt aaa gaa tca aaa ggg aat aag   1267
Ser Ala Lys Gln Phe Asp Ser Gly Leu Lys Glu Ser Lys Gly Asn Lys
        205                 210                 215

aaa tcc aag gaa cct tat gga aag aaa agg ccc atg gaa tct tcg act   1315
Lys Ser Lys Glu Pro Tyr Gly Lys Lys Arg Pro Met Glu Ser Ser Thr
    220                 225                 230

tat tct ctg att gat gat gat gat gat gat gat gat gat gat gac aac   1363
Tyr Ser Leu Ile Asp Asp Asp Asp Asp Asp Asp Asp Asp Asp Asp Asn
235                 240                 245                 250

gac acc agt ggc cat gaa act cct ag gttcgtttcc aactgtttct          1409
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Asp Thr Ser Gly His Glu Thr Pro Ar
                255

gctactagtt tgttgttttc tctaagggtt ctcaagttta ccactgctgg ttactgcaat 1469

tttgttgtga catgacaatc tggtacataa tagaatgaga tgtattgtaa ttgctcaact 1529

tctttctctc atag g gag tgg tct tgg gaa aaa tct cca tca caa agt tca 1580
                g Glu Trp Ser Trp Glu Lys Ser Pro Ser Gln Ser Ser
                  260                 265                 270

agg cgc cgt aag gtattcttgc ttactcccgc tactgtatat cttgcaattg       1632
Arg Arg Arg Lys
            275

cagtttttac gtagtcatta tagtccttaa gaaatttaca ccagcagaag catgactcat 1692

tttctaaacc ttcttgttat ctcccaacag aaaattttat gaattcctta aaaagacttc 1752

agttttcgaa cgtttgattc ctctctagat gaactgcagg atttatactt gccaggaaaa 1812

cttcctactt gactatatca tttatttggc ttctttaata ttgtctttac tccaactcat 1872

ttgttatgtt gtttttctta cttattgatg atattcccta aaaaaactat ag aaa tca 1930
                                                           Lys Ser

gag gac aca gtg ata aat gtg gat gaa gaa gaa gct cag cct tca aca   1978
Glu Asp Thr Val Ile Asn Val Asp Glu Glu Glu Ala Gln Pro Ser Thr
        280                 285                 290

gtg gcg gag caa gcg gct gaa ctg cct gaa gg gtaaatgtga cctattttct  2030
Val Ala Glu Gln Ala Ala Glu Leu Pro Glu Gl
    295                 300

ctttag c ctc att aag tta caa ctg gct ata tat aaa cta ata gtt gat  2079
       y Leu Ile Lys Leu Gln Leu Ala Ile Tyr Lys Leu Ile Val Asp
         305                 310                 315

aaa aca tgc agc tta cag gaa gat ata tgc tac cca aca ag gtaaatctat 2130
Lys Thr Cys Ser Leu Gln Glu Asp Ile Cys Tyr Pro Thr ArSe
    320                 325                 330      e

ctcaagactg atctaggcta acttcctgta aatttgtaac cctcaaaaga tttaatgctt 2190

ggtgattcag ggatgatcct cactttgttc aagtttgtct taaagatctt gaatgccttg 2250

cacctcgaga atatctgaca tcgccggtta tgaatttcta catgaggtat tttttggagt 2310

gatagacttg ccatatatgt catcttatat tatgctagcg ctatttgcat gttatttata 2370

taactattgt cctgttttct tttggtag g ttc ttg cag cag cag ata tca tca   2423
                                g Phe Leu Gln Gln Gln Ile Ser S
                                  h       335                 340

tcg aat caa atc tct gct gat tgt cac ttc ttt aat acc tat ttc tac   2471
r Ser Asn Gln Ile Ser Ala Asp Cys His Phe Phe Asn Thr Tyr Phe T
                345                 350                 355
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aag aag ctc agt gac gct gtt acg tac aag gtgattagaa aaatgtgatc     2521
r Lys Lys Leu Ser Asp Ala Val Thr Tyr Lys
              360                 365

ctttaaaaat aattatctgt tggcattctt gcgattcaaa tttttatcat tgttatttat 2581

gttaactggt ctatttatct tgtcctttca atgaaatag ggg aat gac aag gat    2635
                                          Gly Asn Asp Lys A
                                                      370

gcc ttc ttt gtg agg ttc agg cgg tgg tgg aag ggt att gat cta ttt   2683
p Ala Phe Phe Val Arg Phe Arg Arg Trp Trp Lys Gly Ile Asp Leu P
              375                 380                 385

cgt aag gct tat att ttc ata cca ata cat gaa ga gtaagtatct         2728
e Arg Lys Ala Tyr Ile Phe Ile Pro Ile His Glu
          390                 395

ttccttttag cactctactt tcgatttttt cgcaagagtt ctcaagaatt cagattcttg 2788

taccatgttt cag t ctc cac tgg agc ctt gtg ata gtt tgc atc cct gat  2838
               r Leu His Trp Ser Leu Val Ile Val Cys Ile Pro Asp
                 e 400s                405                 410

aag aaa gat gaa tcg ggg ttg act ata ctt cac ctt gat tct cta gga   2886
Lys Lys Asp Glu Ser Gly Leu Thr Ile Leu His Leu Asp Ser Leu Gly
                415                 420                 425

ctt cac tcg aga aaa tca att gtt gaa aat gta aaa ag gtgagatgct     2934
Leu His Ser Arg Lys Ser Ile Val Glu Asn Val Lys Ar
            430                 435

aggggcttta cccgtgactt tatgttctca catgcttgac gttgtatgca tatggtttca 2994

gttcataaaa ggaaaaatta ttacactggc ttgaaaatgt acgacattta ctagtttcta 3054

tgtcaatttg ttgtag g ttt cta aaa gac gaa tgg aat tat ttg aat caa   3104
                  g Phe Leu Lys Asp Glu Trp Asn Tyr Leu Asn Gln
                    440                 445                 450

gat gac tat tcc ttg gat ctg cct atc tca gaa aaa gta tgg aaa aac   3152
Asp Asp Tyr Ser Leu Asp Leu Pro Ile Ser Glu Lys Val Trp Lys Asn
                455                 460                 465

ctc cct cgt agg atc agc gaa gct gtt gtt cag gtcagtcttt taccttctta 3205
Leu Pro Arg Arg Ile Ser Glu Ala Val Val Gln
            470                 475

atcccatgat tcaaggaact ttgtttatac ggtttcttcg gaaatatgat tatattcaga 3265

cactagaacc acaggaagtt caattcgtct tatgatatta ttctctttgt gcaaccag   3323

gtt ccg cag cag aaa aac gat ttt gat tgt ggt ccg ttt gtg ctc ttc   3371
Val Pro Gln Gln Lys Asn Asp Phe Asp Cys Gly Pro Phe Val Leu Phe
        480                 485                 490
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ttc att aaa cgg ttc att gaa gag gcg cct caa agg ctg aaa agg aaa 3419
Phe Ile Lys Arg Phe Ile Glu Glu Ala Pro Gln Arg Leu Lys Arg Lys
495 500 505

gac ctg gga atg gtgagtaatc tcaaactctt ttcctgatac cgaatcacat 3471
Asp Leu Gly Met
510

atcttcttct tactcttgtc taaacttgtg tcctcaatgt atccag ttc gac aag 3526
Phe Asp Lys
515

aag tgg ttt aga ccc gat gaa gcc tct gct ctg aga atc aaa atc cga 3574
Lys Trp Phe Arg Pro Asp Glu Ala Ser Ala Leu Arg Ile Lys Ile Arg
520 525 530

aac acg ctc atc gag cta ttc cgt gtc agt gac cag aca gag taa 3619
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Val Pro Glu Leu Glu Ile Val Asn Thr Thr Lys Pro Thr Pro Pro Pro
35 40 45

Pro Pro Thr Phe Phe Ser Asp Asp Gln Thr Asp Ser Pro Lys Leu Leu
50 55 60

Thr Asp Arg Asp Leu Asp Glu Gln Leu Glu Arg Lys Lys Ala Ile Leu
65 70 75 80

Thr Leu Gly Pro Gly Leu Pro Asp Lys Gly Glu Lys Ile Arg Leu Lys
85 90 95

Ile Ala Asp Leu Glu Glu Glu Lys Gln Arg Ser Asp Val Leu Pro Gln
100 105 110

Gly Asn Ala Val Ser Lys Asp Thr Ser Arg Gly Asn Ala Asp Ser Lys
115 120 125

Asp Thr Ser Arg Gln Gly Asn Ala Asp Ser Lys Glu Val Ser Arg Ser
130 135 140

Thr Phe Ser Ala Val Phe Ser Lys Pro Lys Thr Asp Ser Gln Ser Lys

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145                 150                 155                 160

Lys Ala Phe Gly Lys Glu Leu Glu Asp Leu Gly Cys Glu Arg Arg Lys
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His Lys Ala Gly Arg Lys Pro Val Thr Arg Leu Ser Asn Gly Trp Arg
            180                 185                 190

Leu Leu Pro Asp Val Gly Lys Ala Glu His Ser Ala Lys Gln Phe Asp
        195                 200                 205

Ser Gly Leu Lys Glu Ser Lys Gly Asn Lys Lys Ser Lys Glu Pro Tyr
    210                 215                 220

Gly Lys Lys Arg Pro Met Glu Ser Ser Thr Tyr Ser Leu Ile Asp Asp
225                 230                 235                 240

Asp Asp Asp Asp Asp Asp Asp Asp Asp Asn Asp Thr Ser Gly His Glu
                245                 250                 255

Thr Pro Arg Glu Trp Ser Trp Glu Lys Ser Pro Ser Gln Ser Ser Arg
            260                 265                 270

Arg Arg Lys Lys Ser Glu Asp Thr Val Ile Asn Val Asp Glu Glu Glu
        275                 280                 285

Ala Gln Pro Ser Thr Val Ala Glu Gln Ala Ala Glu Leu Pro Glu Gly
    290                 295                 300

Leu Ile Lys Leu Gln Leu Ala Ile Tyr Lys Leu Ile Val Asp Lys Thr
305                 310                 315                 320

Cys Ser Leu Gln Glu Asp Ile Cys Tyr Pro Thr ArSeg Phe Leu Gln
                325                 330         e         335

Gln Gln Ile Ser Sr Ser Asn Gln Ile Ser Ala Asp Cys His Phe Phe
               340e                 345                 350

Asn Thr Tyr Phe Tr Lys Lys Leu Ser Asp Ala Val Thr Tyr Lys Gly
              355y                 360                 365

Asn Asp Lys Ap Ala Phe Phe Val Arg Phe Arg Arg Trp Trp Lys Gly
               370                 375                 380

Ile Asp Leu Pe Arg Lys Ala Tyr Ile Phe Ile Pro Ile His Glu r
              385                 390                 395u

Leu His Trp Ser Leu Val Ile Val Cys Ile Pro Asp Lys Lys Asp Glu
            400                 405                 410

Ser Gly Leu Thr Ile Leu His Leu Asp Ser Leu Gly Leu His Ser Arg
        415                 420                 425

Lys Ser Ile Val Glu Asn Val Lys Arg Phe Leu Lys Asp Glu Trp Asn
    430                 435                 440

Tyr Leu Asn Gln Asp Asp Tyr Ser Leu Asp Leu Pro Ile Ser Glu Lys
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445                 450                 455                 460

Val Trp Lys Asn Leu Pro Arg Arg Ile Ser Glu Ala Val Val Gln Val
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Pro Gln Gln Lys Asn Asp Phe Asp Cys Gly Pro Phe Val Leu Phe Phe
            480                 485                 490

Ile Lys Arg Phe Ile Glu Glu Ala Pro Gln Arg Leu Lys Arg Lys Asp
        495                 500                 505

Leu Gly Met Phe Asp Lys Lys Trp Phe Arg Pro Asp Glu Ala Ser Ala
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Asp Gln Thr Glu


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Gly Thr Arg Leu Arg Pro Leu Thr Leu Ser Phe Pro Lys Pro Leu Val
                15                  20                  25

gat ttt gct aat aaa ccc atg atc ctt cat cag ata gag gct ctt aag    147
Asp Phe Ala Asn Lys Pro Met Ile Leu His Gln Ile Glu Ala Leu Lys
            30                  35                  40

gca gtt gga gtt gat gaa gtg gtt ttg gcc atc aat tat cag cca gag    195
Ala Val Gly Val Asp Glu Val Val Leu Ala Ile Asn Tyr Gln Pro Glu
        45                  50                  55

gtg atg ctg aac ttc ttg aag gac ttt gag acc aag ctg gaa atc aaa    243
Val Met Leu Asn Phe Leu Lys Asp Phe Glu Thr Lys Leu Glu Ile Lys
    60                  65                  70

atc act tgc tca caa gag acc gag cca cta ggt acc gct ggt cct ctg    291
Ile Thr Cys Ser Gln Glu Thr Glu Pro Leu Gly Thr Ala Gly Pro Leu
75                  80                  85                  90

gct cta gcg aga gac aaa ttg ctt gat gga tct gga gag ccc ttc ttt    339
Ala Leu Ala Arg Asp Lys Leu Leu Asp Gly Ser Gly Glu Pro Phe Phe
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              95                 100                 105

gtt ctt aac agt gat gtg att agt gag tac cct ctt aaa gaa atg ctt     387
Val Leu Asn Ser Asp Val Ile Ser Glu Tyr Pro Leu Lys Glu Met Leu
            110                 115                 120

gag ttt cac aaa tct cac ggt ggg gaa gcc tcc ata atg gta aca aag     435
Glu Phe His Lys Ser His Gly Gly Glu Ala Ser Ile Met Val Thr Lys
        125                 130                 135

gtg gat gaa ccg tcg aaa tat gga gtg gtt gtt atg gaa gaa agc act     483
Val Asp Glu Pro Ser Lys Tyr Gly Val Val Val Met Glu Glu Ser Thr
    140                 145                 150

gga aga gtg gag aag ttt gtg gaa aag cca aaa ctg tat gta ggt aac     531
Gly Arg Val Glu Lys Phe Val Glu Lys Pro Lys Leu Tyr Val Gly Asn
155                 160                 165                 170

aag atc aac gct ggg att tat ctt ctg aac cca tct gtt ctt gat aag     579
Lys Ile Asn Ala Gly Ile Tyr Leu Leu Asn Pro Ser Val Leu Asp Lys
                175                 180                 185

att gag cta aga ccg act tca atc gaa aaa gag act ttc cct aag att     627
Ile Glu Leu Arg Pro Thr Ser Ile Glu Lys Glu Thr Phe Pro Lys Ile
            190                 195                 200

gca gca gcg caa ggg ctc tat gct atg gtg cta cca ggg ttt tgg atg     675
Ala Ala Ala Gln Gly Leu Tyr Ala Met Val Leu Pro Gly Phe Trp Met
        205                 210                 215

gac att ggg caa ccc cgt gac tac ata acg ggt ttg aga ctc tac tta     723
Asp Ile Gly Gln Pro Arg Asp Tyr Ile Thr Gly Leu Arg Leu Tyr Leu
    220                 225                 230

gac tcc ctt agg aag aaa tct cct gcc aaa tta acc agt ggg cca cac     771
Asp Ser Leu Arg Lys Lys Ser Pro Ala Lys Leu Thr Ser Gly Pro His
235                 240                 245                 250

ata gtt ggg aat gtt ctt gtt gac gaa acc gct aca att ggg gaa gga     819
Ile Val Gly Asn Val Leu Val Asp Glu Thr Ala Thr Ile Gly Glu Gly
                255                 260                 265

tgt ttg att gga cca gac gtt gcc att ggt cca ggc tgc att gtt gag     867
Cys Leu Ile Gly Pro Asp Val Ala Ile Gly Pro Gly Cys Ile Val Glu
            270                 275                 280

tca gga gtc aga ctc tcc cga tgc acg gtc atg cgt gga gtc cgc atc     915
Ser Gly Val Arg Leu Ser Arg Cys Thr Val Met Arg Gly Val Arg Ile
        285                 290                 295

aag aag cat gcg tgt atc tcg agc agt atc atc ggg tgg cac tca acg     963
Lys Lys His Ala Cys Ile Ser Ser Ser Ile Ile Gly Trp His Ser Thr
    300                 305                 310

gtt ggt caa tgg gcc agg atc gag aac atg acg atc ctc ggt gag gat     1011
Val Gly Gln Trp Ala Arg Ile Glu Asn Met Thr Ile Leu Gly Glu Asp
315                 320                 325                 330
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gtt cat gtg agc gat gag atc tat agc aat gga gga gtt gtt ttg cca    1059
Val His Val Ser Asp Glu Ile Tyr Ser Asn Gly Gly Val Val Leu Pro
                335                 340                 345

cac aag gag atc aaa tca aac atc ttg aag cca gag ata gtg atg tga    1107
His Lys Glu Ile Lys Ser Asn Ile Leu Lys Pro Glu Ile Val Met
            350                 355                 360

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            20                  25                  30

Met Ile Leu His Gln Ile Glu Ala Leu Lys Ala Val Gly Val Asp Glu
        35                  40                  45

Val Val Leu Ala Ile Asn Tyr Gln Pro Glu Val Met Leu Asn Phe Leu
    50                  55                  60

Lys Asp Phe Glu Thr Lys Leu Glu Ile Lys Ile Thr Cys Ser Gln Glu
 65                  70                  75                  80

Thr Glu Pro Leu Gly Thr Ala Gly Pro Leu Ala Leu Ala Arg Asp Lys
                 85                  90                  95

Leu Leu Asp Gly Ser Gly Glu Pro Phe Phe Val Leu Asn Ser Asp Val
            100                 105                 110

Ile Ser Glu Tyr Pro Leu Lys Glu Met Leu Glu Phe His Lys Ser His
        115                 120                 125

Gly Gly Glu Ala Ser Ile Met Val Thr Lys Val Asp Glu Pro Ser Lys
    130                 135                 140

Tyr Gly Val Val Val Met Glu Glu Ser Thr Gly Arg Val Glu Lys Phe
145                 150                 155                 160

Val Glu Lys Pro Lys Leu Tyr Val Gly Asn Lys Ile Asn Ala Gly Ile
                165                 170                 175

Tyr Leu Leu Asn Pro Ser Val Leu Asp Lys Ile Glu Leu Arg Pro Thr
            180                 185                 190

Ser Ile Glu Lys Glu Thr Phe Pro Lys Ile Ala Ala Ala Gln Gly Leu
        195                 200                 205
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Tyr Ala Met Val Leu Pro Gly Phe Trp Met Asp Ile Gly Gln Pro Arg
    210                 215                 220

Asp Tyr Ile Thr Gly Leu Arg Leu Tyr Leu Asp Ser Leu Arg Lys Lys
225                 230                 235                 240

Ser Pro Ala Lys Leu Thr Ser Gly Pro His Ile Val Gly Asn Val Leu
                245                 250                 255

Val Asp Glu Thr Ala Thr Ile Gly Glu Gly Cys Leu Ile Gly Pro Asp
            260                 265                 270

Val Ala Ile Gly Pro Gly Cys Ile Val Glu Ser Gly Val Arg Leu Ser
        275                 280                 285

Arg Cys Thr Val Met Arg Gly Val Arg Ile Lys Lys His Ala Cys Ile
    290                 295                 300

Ser Ser Ser Ile Ile Gly Trp His Ser Thr Val Gly Gln Trp Ala Arg
305                 310                 315                 320

Ile Glu Asn Met Thr Ile Leu Gly Glu Asp Val His Val Ser Asp Glu
                325                 330                 335

Ile Tyr Ser Asn Gly Gly Val Val Leu Pro His Lys Glu Ile Lys Ser
            340                 345                 350

Asn Ile Leu Lys Pro Glu Ile Val Met
        355                 360


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         Met Lys Ala Thr Leu Ala Ala Pro Ser Ser Leu Thr Ser Leu
           1               5                  10

cct tat cga acc aac tct tct ttc ggc tca aag tca tcg ctt ctc ttt    98
Pro Tyr Arg Thr Asn Ser Ser Phe Gly Ser Lys Ser Ser Leu Leu Phe
 15                  20                  25                  30

cgg tct cca tcc tcc tcc tcc tca gtc tct atg acg aca acg cgt gga   146
Arg Ser Pro Ser Ser Ser Ser Ser Val Ser Met Thr Thr Thr Arg Gly
                 35                  40                  45

aac gtg gct gtg gcg gct gct gct aca tcc act gag gcg cta aga aaa   194
Asn Val Ala Val Ala Ala Ala Ala Thr Ser Thr Glu Ala Leu Arg Lys
             50                  55                  60
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gga ata gcg gag ttc tac aat gaa act tcg ggt ttg tgg gaa gag att   242
Gly Ile Ala Glu Phe Tyr Asn Glu Thr Ser Gly Leu Trp Glu Glu Ile
         65                  70                  75

tgg gga gat cat atg cat cat ggc ttt tat gac cct gat tct tct gtt   290
Trp Gly Asp His Met His His Gly Phe Tyr Asp Pro Asp Ser Ser Val
     80                  85                  90

caa ctt tct gat tct ggt cac aag gaa gct cag atc cgt atg att gaa   338
Gln Leu Ser Asp Ser Gly His Lys Glu Ala Gln Ile Arg Met Ile Glu
 95                 100                 105                 110

gag tct ctc cgt ttc gcc ggt gtt act gat gaa gag gag gag aaa aag   386
Glu Ser Leu Arg Phe Ala Gly Val Thr Asp Glu Glu Glu Glu Lys Lys
                115                 120                 125

ata aag aaa gta gtg gat gtt ggg tgt ggg att gga gga agc tca aga   434
Ile Lys Lys Val Val Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg
            130                 135                 140

tat ctt gcc tct aaa ttt gga gct gaa tgc att ggc att act ctc agc   482
Tyr Leu Ala Ser Lys Phe Gly Ala Glu Cys Ile Gly Ile Thr Leu Ser
        145                 150                 155

cct gtt cag gcc aag aga gcc aat gat ctc gcg gct gct caa tca ctc   530
Pro Val Gln Ala Lys Arg Ala Asn Asp Leu Ala Ala Ala Gln Ser Leu
    160                 165                 170

tct cat aag gct tcc ttc caa gtt gcg gat gcg ttg gat cag cca ttc   578
Ser His Lys Ala Ser Phe Gln Val Ala Asp Ala Leu Asp Gln Pro Phe
175                 180                 185                 190

gaa gat gga aaa ttc gat cta gtg tgg tcg atg gag agt ggt gag cat   626
Glu Asp Gly Lys Phe Asp Leu Val Trp Ser Met Glu Ser Gly Glu His
                195                 200                 205

atg cct gac aag gcc aag ttt gta aaa gag ttg gta cgt gtg gcg gct   674
Met Pro Asp Lys Ala Lys Phe Val Lys Glu Leu Val Arg Val Ala Ala
            210                 215                 220

cca gga ggt agg ata ata ata gtg aca tgg tgc cat aga aat cta tct   722
Pro Gly Gly Arg Ile Ile Ile Val Thr Trp Cys His Arg Asn Leu Ser
        225                 230                 235

gcg ggg gag gaa gct ttg cag ccg tgg gag caa aac atc ttg gac aaa   770
Ala Gly Glu Glu Ala Leu Gln Pro Trp Glu Gln Asn Ile Leu Asp Lys
    240                 245                 250

atc tgt aag acg ttc tat ctc ccg gct tgg tgc tcc acc gat gat tat   818
Ile Cys Lys Thr Phe Tyr Leu Pro Ala Trp Cys Ser Thr Asp Asp Tyr
255                 260                 265                 270

gtc aac ttg ctt caa tcc cat tct ctc cag gat att aag tgt gcg gat   866
Val Asn Leu Leu Gln Ser His Ser Leu Gln Asp Ile Lys Cys Ala Asp
                275                 280                 285
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tgg tca gag aac gta gct cct ttc tgg cct gcg gtt ata cgg act gca    914
Trp Ser Glu Asn Val Ala Pro Phe Trp Pro Ala Val Ile Arg Thr Ala
            290                 295                 300

tta aca tgg aag ggc ctt gtg tct ctg ctt cgt agt ggt atg aaa agt    962
Leu Thr Trp Lys Gly Leu Val Ser Leu Leu Arg Ser Gly Met Lys Ser
        305                 310                 315

att aaa gga gca ttg aca atg cca ttg atg att gaa ggt tac aag aaa   1010
Ile Lys Gly Ala Leu Thr Met Pro Leu Met Ile Glu Gly Tyr Lys Lys
    320                 325                 330

ggt gtc att aag ttt ggt atc atc act tgc cag aag cca ctc taa       1055
Gly Val Ile Lys Phe Gly Ile Ile Thr Cys Gln Lys Pro Leu
335                 340                 345

gtctaaagct atacta                                                 1071


<210> 26
<211> 348
<212> PRT
<213> Arabidopsis thaliana

<400> 26
Met Lys Ala Thr Leu Ala Ala Pro Ser Ser Leu Thr Ser Leu Pro Tyr
  1               5                  10                  15

Arg Thr Asn Ser Ser Phe Gly Ser Lys Ser Ser Leu Leu Phe Arg Ser
             20                  25                  30

Pro Ser Ser Ser Ser Ser Val Ser Met Thr Thr Thr Arg Gly Asn Val
         35                  40                  45

Ala Val Ala Ala Ala Ala Thr Ser Thr Glu Ala Leu Arg Lys Gly Ile
     50                  55                  60

Ala Glu Phe Tyr Asn Glu Thr Ser Gly Leu Trp Glu Glu Ile Trp Gly
 65                  70                  75                  80

Asp His Met His His Gly Phe Tyr Asp Pro Asp Ser Ser Val Gln Leu
                 85                  90                  95

Ser Asp Ser Gly His Lys Glu Ala Gln Ile Arg Met Ile Glu Glu Ser
            100                 105                 110

Leu Arg Phe Ala Gly Val Thr Asp Glu Glu Glu Glu Lys Lys Ile Lys
        115                 120                 125

Lys Val Val Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Tyr Leu
    130                 135                 140

Ala Ser Lys Phe Gly Ala Glu Cys Ile Gly Ile Thr Leu Ser Pro Val
145                 150                 155                 160

Gln Ala Lys Arg Ala Asn Asp Leu Ala Ala Ala Gln Ser Leu Ser His
                165                 170                 175
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Lys Ala Ser Phe Gln Val Ala Asp Ala Leu Asp Gln Pro Phe Glu Asp
            180                 185                 190

Gly Lys Phe Asp Leu Val Trp Ser Met Glu Ser Gly Glu His Met Pro
        195                 200                 205

Asp Lys Ala Lys Phe Val Lys Glu Leu Val Arg Val Ala Ala Pro Gly
    210                 215                 220

Gly Arg Ile Ile Ile Val Thr Trp Cys His Arg Asn Leu Ser Ala Gly
225                 230                 235                 240

Glu Glu Ala Leu Gln Pro Trp Glu Gln Asn Ile Leu Asp Lys Ile Cys
                245                 250                 255

Lys Thr Phe Tyr Leu Pro Ala Trp Cys Ser Thr Asp Asp Tyr Val Asn
            260                 265                 270

Leu Leu Gln Ser His Ser Leu Gln Asp Ile Lys Cys Ala Asp Trp Ser
        275                 280                 285

Glu Asn Val Ala Pro Phe Trp Pro Ala Val Ile Arg Thr Ala Leu Thr
    290                 295                 300

Trp Lys Gly Leu Val Ser Leu Leu Arg Ser Gly Met Lys Ser Ile Lys
305                 310                 315                 320

Gly Ala Leu Thr Met Pro Leu Met Ile Glu Gly Tyr Lys Lys Gly Val
                325                 330                 335

Ile Lys Phe Gly Ile Ile Thr Cys Gln Lys Pro Leu
            340                 345
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<210> 27
<211> 768
<212> DNA
<213> Arabidopsis thaliana

<220>
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<222> (3)..(752)

<400> 27

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   Met Lys Phe Asn Val Ala Asn Pro Thr Thr Gly Cys Gln Lys Lys
     1               5                  10                  15

ctc gag atc gac gat gac cag aaa cta cgt gcg ttt tac gac aag aga      95
Leu Glu Ile Asp Asp Asp Gln Lys Leu Arg Ala Phe Tyr Asp Lys Arg
                20                  25                  30

atc tct caa gaa gtc agt gga gat gct ttg ggc gag gag ttc aaa gga     143
Ile Ser Gln Glu Val Ser Gly Asp Ala Leu Gly Glu Glu Phe Lys Gly
            35                  40                  45
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tac gtt ttc aag atc aag ggt ggt tgc gat aag caa ggt ttc cca atg    191
Tyr Val Phe Lys Ile Lys Gly Gly Cys Asp Lys Gln Gly Phe Pro Met
         50                  55                  60

aag cag gga gtt ttg act cca ggc cgt gtt cgc ctt ttg ctt cac cga    239
Lys Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His Arg
    65                  70                  75

gga act cct tgc ttc aga gga cat gga agg aga act ggt gag agg aga    287
Gly Thr Pro Cys Phe Arg Gly His Gly Arg Arg Thr Gly Glu Arg Arg
80                  85                  90                  95

aga aag tct gtt cgt ggt tgc att gtg agc cct gat ctc tct gtt ctg    335
Arg Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val Leu
                100                 105                 110

aac ctt gtc att gtg aag aag ggt gag aac gat ctt cct ggg ctt acc    383
Asn Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr
            115                 120                 125

gat cat gag agc aag atg aga gga cca aag aga gcc tcc aag atc cgt    431
Asp His Glu Ser Lys Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg
        130                 135                 140

aaa ctg ttt aac ctc aag aag gaa gat gat gtc agg acc tat gtc aac    479
Lys Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn
    145                 150                 155

act tac cgc cgc aag ttc aca aac aag aag ggc aag gaa gtt agc aaa    527
Thr Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys
160                 165                 170                 175

gcc cct aag atc cag agg ctt gtg acc cca ttg act ctt cag agg aag    575
Ala Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys
                180                 185                 190

aga gct aga att gct gac aag aag aag aaa att gct aag gct aat tct    623
Arg Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser
            195                 200                 205

gat gct gct gat tac cag aag ctt ctc gcc tcg agg ttg aag gaa cag    671
Asp Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln
        210                 215                 220

cgt gac agg agg agt gag agt ttg gca aaa gag agg tcg aga ctc tct    719
Arg Asp Arg Arg Ser Glu Ser Leu Ala Lys Glu Arg Ser Arg Leu Ser
    225                 230                 235

tct gct gct gcc aag ccc tct gtc aca gct taa aaaagcttga gattca      768
Ser Ala Ala Ala Lys Pro Ser Val Thr Ala
240                 245                 250

<210> 28
<211> 249
<212> PRT
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<213> Arabidopsis thaliana

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Met Lys Phe Asn Val Ala Asn Pro Thr Thr Gly Cys Gln Lys Lys Leu
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Glu Ile Asp Asp Asp Gln Lys Leu Arg Ala Phe Tyr Asp Lys Arg Ile
20 25 30

Ser Gln Glu Val Ser Gly Asp Ala Leu Gly Glu Glu Phe Lys Gly Tyr
35 40 45

Val Phe Lys Ile Lys Gly Gly Cys Asp Lys Gln Gly Phe Pro Met Lys
50 55 60

Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His Arg Gly
65 70 75 80

Thr Pro Cys Phe Arg Gly His Gly Arg Arg Thr Gly Glu Arg Arg Arg
85 90 95

Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val Leu Asn
100 105 110

Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr Asp
115 120 125

His Glu Ser Lys Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg Lys
130 135 140

Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn Thr
145 150 155 160

Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys Ala
165 170 175

Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys Arg
180 185 190

Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser Asp
195 200 205

Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln Arg
210 215 220

Asp Arg Arg Ser Glu Ser Leu Ala Lys Glu Arg Ser Arg Leu Ser Ser
225 230 235 240

Ala Ala Ala Lys Pro Ser Val Thr Ala
245

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<211> 1201
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<220>
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<222> (1103)..(1196)

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Met Ala Glu Gln
1

ctctaagctt atcctcgttt tatgatctat tgatccttat tcactcaaat gattctaata 115

ctcttctctt ttctctgtca ctaattttca g act gag aaa gct ttt ctt aag 167
Thr Glu Lys Ala Phe Leu Lys
5 10

cag cct aag gtc ttc ctt ag gtaattttgc gattcgattt ctctctgttc 217
Gln Pro Lys Val Phe Leu Se
15

tctattgttt cattgtattt aagttccaag ttgtttatat tgttcattgt ttctgattta 277

tcaag c tcg aag aaa tct gga aag gga aag aga cct gga aaa ggt gga 325
r Ser Lys Lys Ser Gly Lys Gly Lys Arg Pro Gly Lys Gly Gly
20 25 30

aac cgt ttc tgg aag aac att ggt ttg ggc ttc aag act cct cgt gaa 373
Asn Arg Phe Trp Lys Asn Ile Gly Leu Gly Phe Lys Thr Pro Arg Glu
35 40 45

gcc att gat g gtatgtttaa gcttttaact cgttataata gataaggaac 423
Ala Ile Asp G
50

tcttggattg tgttgttcat atagtcgata gatttcaaat gctattttgt cttgtagaat 483

cttaagcttt ggtttagtga gttctgattc ttcagcttta tctggatcta cattactgtt 543

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tcagtgatgc aaatgttatc agtagatttt gaattagtag gatgtcactg atttgaatat 603

gtgatcaagc ttcatagaaa cctgcatcat tctctatata cctttaagtc agattctcag 663

gttattgtgt atttgtgtgg aacag ga gct tac gtt gac aag aaa tgc ccc   714
                              ly Ala Tyr Val Asp Lys Lys Cys Pro
                                             55                  60

ttc act gga act gtt tcc att aga ggt cgt atc tta gct ggt act tgc   762
Phe Thr Gly Thr Val Ser Ile Arg Gly Arg Ile Leu Ala Gly Thr Cys
                65                  70                  75

cac agt gcg aaa atg cag agg acc att atc gtg cga agg gat tac ctt   810
His Ser Ala Lys Met Gln Arg Thr Ile Ile Val Arg Arg Asp Tyr Leu
            80                  85                  90

cac ttt gtg aag aag tat cag ag gtaaattcat acattctcat acttctttcc   863
His Phe Val Lys Lys Tyr Gln Ar
        95

atagagtctt acacattgat gtttaagaaa gtaatatcct ttttgttctt ag g tat   919
                                                          g Tyr
                                                            100

gag aag agg cat tca aac att ccg gct cat gtc tca cca tgc ttc cgt   967
Glu Lys Arg His Ser Asn Ile Pro Ala His Val Ser Pro Cys Phe Arg
            105                 110                 115

gtt aag gaa gga gac cat atc atc att ggc caa tgc ag gttatgatct     1015
Val Lys Glu Gly Asp His Ile Ile Ile Gly Gln Cys Ar
        120                 125

gattcaaacc tacaaattgt ctccattgat tctgattatc gtgaatttgt tttgatcttt 1075

ttgtttgtta atgattgata atttcag g cca ttg tcg aag aca gtg agg ttc   1127
                              g Pro Leu Ser Lys Thr Val Arg Phe
                              130                 135

aat gtg ttg aag gtg ata cca gct ggg tct tct tct tca ttt gga aag   1175
Asn Val Leu Lys Val Ile Pro Ala Gly Ser Ser Ser Ser Phe Gly Lys
    140                 145                 150

aag gca ttc act gga atg taa gctgc                                 1201
Lys Ala Phe Thr Gly Met
155                 160


<210> 30
<211> 160
<212> PRT
<213> Arabidopsis thaliana

<400> 30
Met Ala Glu Gln Thr Glu Lys Ala Phe Leu Lys Gln Pro Lys Val
  1               5                  10                  15
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Phe Leu Ser Ser Lys Lys Ser Gly Lys Gly Lys Arg Pro Gly Lys Gly
20 25 30

Gly Asn Arg Phe Trp Lys Asn Ile Gly Leu Gly Phe Lys Thr Pro Arg
35 40 45

Glu Ala Ile Asp Gly Ala Tyr Val Asp Lys Lys Cys Pro Phe Thr Gly
50 55 60

Thr Val Ser Ile Arg Gly Arg Ile Leu Ala Gly Thr Cys His Ser Ala
65 70 75 8

Lys Met Gln Arg Thr Ile Ile Val Arg Arg Asp Tyr Leu His Phe Val
85 90 95

Lys Lys Tyr Gln Arg Tyr Glu Lys Arg His Ser Asn Ile Pro Ala His
100 105 110

Val Ser Pro Cys Phe Arg Val Lys Glu Gly Asp His Ile Ile Ile Gly
115 120 125

Gln Cys Arg Pro Leu Ser Lys Thr Val Arg Phe Asn Val Leu Lys Val
130 135 140

Ile Pro Ala Gly Ser Ser Ser Ser Phe Gly Lys Lys Ala Phe Thr Gly
145 150 155 16

Met

<210> 31
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<212> DNA
<213> Arabidopsis thaliana

<220>
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<222> (23)..(1780)

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Met Gly Ser Ile Glu Glu Glu Ala Arg Pro
1 5 10

ctc atc gaa gaa ggt tta att tta cag gaa gtg aaa ttg tat gct gaa 100
Leu Ile Glu Glu Gly Leu Ile Leu Gln Glu Val Lys Leu Tyr Ala Glu
15 20 25

gat ggt tca gtg gac ttt aat gga aac cca cca ttg aag gag aaa aca 148
Asp Gly Ser Val Asp Phe Asn Gly Asn Pro Pro Leu Lys Glu Lys Thr
30 35 40

gga aac tgg aaa gct tgt cct ttt att ctt ggt aat gaa tgt tgt gag 196
Gly Asn Trp Lys Ala Cys Pro Phe Ile Leu Gly Asn Glu Cys Cys Glu
45 50 55

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agg cta gct tac tat ggt att gct ggg aat tta atc act tac ctc acc    244
Arg Leu Ala Tyr Tyr Gly Ile Ala Gly Asn Leu Ile Thr Tyr Leu Thr
    60                  65                  70

act aag ctt cac caa gga aat gtt tct gct gct aca aac gtt acc aca    292
Thr Lys Leu His Gln Gly Asn Val Ser Ala Ala Thr Asn Val Thr Thr
75                  80                  85                  90

tgg caa ggg act tgt tat ctc act cct ctc att gga gct gtt ctg gct    340
Trp Gln Gly Thr Cys Tyr Leu Thr Pro Leu Ile Gly Ala Val Leu Ala
                95                  100                 105

gat gct tac tgg gga cgt tac tgg acc atc gct tgt ttc tcc ggg att    388
Asp Ala Tyr Trp Gly Arg Tyr Trp Thr Ile Ala Cys Phe Ser Gly Ile
            110                 115                 120

tat ttc atc ggg atg tct gcg tta act ctt tca gct tca gtt ccg gca    436
Tyr Phe Ile Gly Met Ser Ala Leu Thr Leu Ser Ala Ser Val Pro Ala
        125                 130                 135

ttg aag cca gcg gaa tgt att ggt gac ttt tgt cca tct gca acg cca    484
Leu Lys Pro Ala Glu Cys Ile Gly Asp Phe Cys Pro Ser Ala Thr Pro
    140                 145                 150

gct cag tat gcg atg ttc ttt ggt ggg ctt tac ctg atc gct ctt gga    532
Ala Gln Tyr Ala Met Phe Phe Gly Gly Leu Tyr Leu Ile Ala Leu Gly
155                 160                 165                 170

act gga ggt atc aaa ccg tgt gtc tca tcc ttc ggt gcc gat cag ttt    580
Thr Gly Gly Ile Lys Pro Cys Val Ser Ser Phe Gly Ala Asp Gln Phe
                175                 180                 185

gat gac acg gac tct cgg gaa cga gtt aga aaa gct tcg ttc ttt aac    628
Asp Asp Thr Asp Ser Arg Glu Arg Val Arg Lys Ala Ser Phe Phe Asn
            190                 195                 200

tgg ttt tac ttc tcc atc aat att gga gca ctt gtg tca tct agt ctt    676
Trp Phe Tyr Phe Ser Ile Asn Ile Gly Ala Leu Val Ser Ser Ser Leu
        205                 210                 215

cta gtt tgg att caa gag aat cgg ggg tgg ggt tta ggg ttt ggg ata    724
Leu Val Trp Ile Gln Glu Asn Arg Gly Trp Gly Leu Gly Phe Gly Ile
    220                 225                 230

cca aca gtg ttc atg gga cta gcc att gca agt ttc ttc ttt ggc aca    772
Pro Thr Val Phe Met Gly Leu Ala Ile Ala Ser Phe Phe Phe Gly Thr
235                 240                 245                 250

cct ctt tat agg ttt cag aaa cct gga gga agc cct ata act cgg att    820
Pro Leu Tyr Arg Phe Gln Lys Pro Gly Gly Ser Pro Ile Thr Arg Ile
                255                 260                 265

tcc caa gtc gtg gtt gct tcg ttc cgg aaa tcg tct gtc aaa gtc cct    868
Ser Gln Val Val Val Ala Ser Phe Arg Lys Ser Ser Val Lys Val Pro
            270                 275                 280

gaa gac gcc aca ctt ctg tat gaa act caa gac aag aac tct gct att    916
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Glu Asp Ala Thr Leu Leu Tyr Glu Thr Gln Asp Lys Asn Ser Ala Ile
        285                 290                 295

gct gga agt aga aaa atc gag cat acc gat gat tgc cag tat ctt gac     964
Ala Gly Ser Arg Lys Ile Glu His Thr Asp Asp Cys Gln Tyr Leu Asp
    300                 305                 310

aaa gcc gct gtt atc tca gaa gaa gaa tcg aaa tcc gga gat tat tcc    1012
Lys Ala Ala Val Ile Ser Glu Glu Glu Ser Lys Ser Gly Asp Tyr Ser
315                 320                 325                 330

aac tcg tgg aga cta tgc acg gtt acg caa gtc gaa gaa ctc aag att    1060
Asn Ser Trp Arg Leu Cys Thr Val Thr Gln Val Glu Glu Leu Lys Ile
                335                 340                 345

ctg atc cga atg ttc cca atc tgg gct tct ggt atc att ttc tca gct    1108
Leu Ile Arg Met Phe Pro Ile Trp Ala Ser Gly Ile Ile Phe Ser Ala
            350                 355                 360

gta tac gca caa atg tcc aca atg ttt gtt caa caa ggc cga gcc atg    1156
Val Tyr Ala Gln Met Ser Thr Met Phe Val Gln Gln Gly Arg Ala Met
        365                 370                 375

aac tgc aaa att gga tca ttc cag ctt cct cct gca gca ctc ggg aca    1204
Asn Cys Lys Ile Gly Ser Phe Gln Leu Pro Pro Ala Ala Leu Gly Thr
    380                 385                 390

ttc gac aca gca agc gtc atc atc tgg gtg ccg ctc tac gac cgg ttc    1252
Phe Asp Thr Ala Ser Val Ile Ile Trp Val Pro Leu Tyr Asp Arg Phe
395                 400                 405                 410

atc gtt ccc tta gca aga aag ttc aca gga gta gac aaa gga ttc act    1300
Ile Val Pro Leu Ala Arg Lys Phe Thr Gly Val Asp Lys Gly Phe Thr
                415                 420                 425

gag ata caa aga atg gga att ggt ctg ttt gtc tct gtt ctc tgt atg    1348
Glu Ile Gln Arg Met Gly Ile Gly Leu Phe Val Ser Val Leu Cys Met
            430                 435                 440

gca gct gca gct atc gtc gaa atc atc cgt ctc cat atg gcc aac gat    1396
Ala Ala Ala Ala Ile Val Glu Ile Ile Arg Leu His Met Ala Asn Asp
        445                 450                 455

ctt gga tta gtc gag tca gga gcc cca gtt ccc ata tcc gtc ttg tgg    1444
Leu Gly Leu Val Glu Ser Gly Ala Pro Val Pro Ile Ser Val Leu Trp
    460                 465                 470

cag att cca cag tac ttc att ctc ggt gca gcc gaa gta ttc tac ttc    1492
Gln Ile Pro Gln Tyr Phe Ile Leu Gly Ala Ala Glu Val Phe Tyr Phe
475                 480                 485                 490

atc ggt cag ctc gag ttc ttc tac gac caa tct cca gat gca atg aga    1540
Ile Gly Gln Leu Glu Phe Phe Tyr Asp Gln Ser Pro Asp Ala Met Arg
                495                 500                 505

agc ttg tgc agt gcc tta gct ctt ttg acc aat gca ctt ggt aac tac    1588
Ser Leu Cys Ser Ala Leu Ala Leu Leu Thr Asn Ala Leu Gly Asn Tyr
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            510                 515                 520

ttg agc tcg ttg atc ctc acg ctc gtg act tat ttt aca aca aga aat    1636
Leu Ser Ser Leu Ile Leu Thr Leu Val Thr Tyr Phe Thr Thr Arg Asn
        525                 530                 535

ggg caa gaa ggt tgg att tcg gat aat ctc aat tca ggt cat ctc gat    1684
Gly Gln Glu Gly Trp Ile Ser Asp Asn Leu Asn Ser Gly His Leu Asp
    540                 545                 550

tac ttc ttc tgg ctc ttg gct ggt ctt agc ctt gtg aac atg gcg gtt    1732
Tyr Phe Phe Trp Leu Leu Ala Gly Leu Ser Leu Val Asn Met Ala Val
555                 560                 565                 570

tac ttc ttc tct gct gct agg tat aag caa aag aaa gct tcg tcg tag    1780
Tyr Phe Phe Ser Ala Ala Arg Tyr Lys Gln Lys Lys Ala Ser Ser
                575                 580                 585

taatgctgtt a                                                        1791


<210> 32
<211> 585
<212> PRT
<213> Arabidopsis thaliana

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Met Gly Ser Ile Glu Glu Glu Ala Arg Pro Leu Ile Glu Glu Gly Leu
  1               5                  10                  15

Ile Leu Gln Glu Val Lys Leu Tyr Ala Glu Asp Gly Ser Val Asp Phe
            20                  25                  30

Asn Gly Asn Pro Pro Leu Lys Glu Lys Thr Gly Asn Trp Lys Ala Cys
        35                  40                  45

Pro Phe Ile Leu Gly Asn Glu Cys Cys Glu Arg Leu Ala Tyr Tyr Gly
    50                  55                  60

Ile Ala Gly Asn Leu Ile Thr Tyr Leu Thr Thr Lys Leu His Gln Gly
65                  70                  75                  80

Asn Val Ser Ala Ala Thr Asn Val Thr Thr Trp Gln Gly Thr Cys Tyr
                85                  90                  95

Leu Thr Pro Leu Ile Gly Ala Val Leu Ala Asp Ala Tyr Trp Gly Arg
            100                 105                 110

Tyr Trp Thr Ile Ala Cys Phe Ser Gly Ile Tyr Phe Ile Gly Met Ser
        115                 120                 125

Ala Leu Thr Leu Ser Ala Ser Val Pro Ala Leu Lys Pro Ala Glu Cys
    130                 135                 140

Ile Gly Asp Phe Cys Pro Ser Ala Thr Pro Ala Gln Tyr Ala Met Phe
145                 150                 155                 160
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Phe Gly Gly Leu Tyr Leu Ile Ala Leu Gly Thr Gly Gly Ile Lys Pro
                165                 170                 175

Cys Val Ser Ser Phe Gly Ala Asp Gln Phe Asp Asp Thr Asp Ser Arg
            180                 185                 190

Glu Arg Val Arg Lys Ala Ser Phe Phe Asn Trp Phe Tyr Phe Ser Ile
        195                 200                 205

Asn Ile Gly Ala Leu Val Ser Ser Ser Leu Leu Val Trp Ile Gln Glu
    210                 215                 220

Asn Arg Gly Trp Gly Leu Gly Phe Gly Ile Pro Thr Val Phe Met Gly
225                 230                 235                 240

Leu Ala Ile Ala Ser Phe Phe Phe Gly Thr Pro Leu Tyr Arg Phe Gln
                245                 250                 255

Lys Pro Gly Gly Ser Pro Ile Thr Arg Ile Ser Gln Val Val Val Ala
            260                 265                 270

Ser Phe Arg Lys Ser Ser Val Lys Val Pro Glu Asp Ala Thr Leu Leu
        275                 280                 285

Tyr Glu Thr Gln Asp Lys Asn Ser Ala Ile Ala Gly Ser Arg Lys Ile
    290                 295                 300

Glu His Thr Asp Asp Cys Gln Tyr Leu Asp Lys Ala Ala Val Ile Ser
305                 310                 315                 320

Glu Glu Glu Ser Lys Ser Gly Asp Tyr Ser Asn Ser Trp Arg Leu Cys
                325                 330                 335

Thr Val Thr Gln Val Glu Glu Leu Lys Ile Leu Ile Arg Met Phe Pro
            340                 345                 350

Ile Trp Ala Ser Gly Ile Ile Phe Ser Ala Val Tyr Ala Gln Met Ser
        355                 360                 365

Thr Met Phe Val Gln Gln Gly Arg Ala Met Asn Cys Lys Ile Gly Ser
    370                 375                 380

Phe Gln Leu Pro Pro Ala Ala Leu Gly Thr Phe Asp Thr Ala Ser Val
385                 390                 395                 400

Ile Ile Trp Val Pro Leu Tyr Asp Arg Phe Ile Val Pro Leu Ala Arg
                405                 410                 415

Lys Phe Thr Gly Val Asp Lys Gly Phe Thr Glu Ile Gln Arg Met Gly
            420                 425                 430

Ile Gly Leu Phe Val Ser Val Leu Cys Met Ala Ala Ala Ala Ile Val
        435                 440                 445

Glu Ile Ile Arg Leu His Met Ala Asn Asp Leu Gly Leu Val Glu Ser
    450                 455                 460
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Gly Ala Pro Val Pro Ile Ser Val Leu Trp Gln Ile Pro Gln Tyr Phe
465                 470                 475                 480

Ile Leu Gly Ala Ala Glu Val Phe Tyr Phe Ile Gly Gln Leu Glu Phe
                485                 490                 495

Phe Tyr Asp Gln Ser Pro Asp Ala Met Arg Ser Leu Cys Ser Ala Leu
            500                 505                 510

Ala Leu Leu Thr Asn Ala Leu Gly Asn Tyr Leu Ser Ser Leu Ile Leu
        515                 520                 525

Thr Leu Val Thr Tyr Phe Thr Thr Arg Asn Gly Gln Glu Gly Trp Ile
    530                 535                 540

Ser Asp Asn Leu Asn Ser Gly His Leu Asp Tyr Phe Phe Trp Leu Leu
545                 550                 555                 560

Ala Gly Leu Ser Leu Val Asn Met Ala Val Tyr Phe Phe Ser Ala Ala
                565                 570                 575

Arg Tyr Lys Gln Lys Lys Ala Ser Ser
            580                 585


&lt;210&gt; 33
&lt;211&gt; 1984
&lt;212&gt; DNA
&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; (20)..(1975)

&lt;400&gt; 33
ttcaccgtcg gcttctcaa atg cag gat att ctc gga tcg gtt cgc cga tcc    52
                     Met Gln Asp Ile Leu Gly Ser Val Arg Arg Ser
                     1               5                   10

ttg gtt ttc cgg tcg tct ttg gcc gga gac gat ggt act agc ggc gga    100
Leu Val Phe Arg Ser Ser Leu Ala Gly Asp Asp Gly Thr Ser Gly Gly
            15                  20                  25

ggt ctt agc gga ttc gtc ggg aag att aac tct agt atc cgt agc tct    148
Gly Leu Ser Gly Phe Val Gly Lys Ile Asn Ser Ser Ile Arg Ser Ser
        30                  35                  40

cga att ggg ctc ttt tct aag ccg cct cca ggg ctt cct gct cct aga    196
Arg Ile Gly Leu Phe Ser Lys Pro Pro Pro Gly Leu Pro Ala Pro Arg
    45                  50                  55

aaa gaa gaa gcg ccg tcg att cgg tgg agg aaa ggg gaa tta atc ggt    244
Lys Glu Glu Ala Pro Ser Ile Arg Trp Arg Lys Gly Glu Leu Ile Gly
60                  65                  70                  75

tgc ggt gct ttt gga aga gtt tac atg gga atg aac ctc gat tcc ggc    292
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Cys Gly Ala Phe Gly Arg Val Tyr Met Gly Met Asn Leu Asp Ser Gly
                 80                  85                  90

gag ctt ctt gca att aaa cag gtt tta atc gct cca agc agt gct tca    340
Glu Leu Leu Ala Ile Lys Gln Val Leu Ile Ala Pro Ser Ser Ala Ser
             95                 100                 105

aag gag aag act cag ggt cac atc cga gag ctt gag gaa gaa gta caa    388
Lys Glu Lys Thr Gln Gly His Ile Arg Glu Leu Glu Glu Glu Val Gln
        110                 115                 120

ctt ctt aag aat ctt tca cat ccg aac atc gtt aga tac ttg ggt act    436
Leu Leu Lys Asn Leu Ser His Pro Asn Ile Val Arg Tyr Leu Gly Thr
    125                 130                 135

gta aga gag agt gat tcg ttg aat att ttg atg gag ttt gtt cct ggt    484
Val Arg Glu Ser Asp Ser Leu Asn Ile Leu Met Glu Phe Val Pro Gly
140                 145                 150                 155

gga tca ata tca tct ttg ttg gag aag ttt gga tct ttt cct gag cct    532
Gly Ser Ile Ser Ser Leu Leu Glu Lys Phe Gly Ser Phe Pro Glu Pro
                160                 165                 170

gtg att att atg tac aca aag caa ctt ctg ctt ggg ctg gaa tat ctt    580
Val Ile Ile Met Tyr Thr Lys Gln Leu Leu Leu Gly Leu Glu Tyr Leu
            175                 180                 185

cac aac aat ggg atc atg cat cga gat att aag ggg gca aat att ttg    628
His Asn Asn Gly Ile Met His Arg Asp Ile Lys Gly Ala Asn Ile Leu
        190                 195                 200

gtc gat aac aaa ggt tgc atc aga ctc gca gat ttt ggt gct tcc aag    676
Val Asp Asn Lys Gly Cys Ile Arg Leu Ala Asp Phe Gly Ala Ser Lys
    205                 210                 215

aaa gtt gta gag cta gct act gta aat ggt gcc aaa tct atg aag ggg    724
Lys Val Val Glu Leu Ala Thr Val Asn Gly Ala Lys Ser Met Lys Gly
220                 225                 230                 235

acg cct tat tgg atg gct cct gaa gtc att ctc cag act ggt cat agc    772
Thr Pro Tyr Trp Met Ala Pro Glu Val Ile Leu Gln Thr Gly His Ser
                240                 245                 250

ttc tct gct gat ata tgg agt gtt ggg tgc act gtg att gag atg gct    820
Phe Ser Ala Asp Ile Trp Ser Val Gly Cys Thr Val Ile Glu Met Ala
            255                 260                 265

acg ggg aag cct ccc tgg agc gag cag tat cag cag ttt gct gct gtc    868
Thr Gly Lys Pro Pro Trp Ser Glu Gln Tyr Gln Gln Phe Ala Ala Val
        270                 275                 280

ctt cat att ggt aga aca aaa gct cat cct cca att cca gaa gac ctc    916
Leu His Ile Gly Arg Thr Lys Ala His Pro Pro Ile Pro Glu Asp Leu
    285                 290                 295

tca cca gag gct aaa gac ttt cta atg aaa tgc tta cac aaa gaa cca    964
Ser Pro Glu Ala Lys Asp Phe Leu Met Lys Cys Leu His Lys Glu Pro
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300 305 310 315

agc ttg aga ctc tct gca acc gaa ttg ctt cag cac ccg ttt gtc act 1012
Ser Leu Arg Leu Ser Ala Thr Glu Leu Leu Gln His Pro Phe Val Thr
320 325 330

gga aag cgc cag gaa cct tat cca gct tac cgt aat tct ctt acg gaa 1060
Gly Lys Arg Gln Glu Pro Tyr Pro Ala Tyr Arg Asn Ser Leu Thr Glu
335 340 345

tgt gga aac cca ata act act caa gga atg aat gtt cgg agt tca ata 1108
Cys Gly Asn Pro Ile Thr Thr Gln Gly Met Asn Val Arg Ser Ser Ile
350 355 360

aat tcg ttg atc agg agg tcg aca tgt tca ggc ttg aag gat gtc tgt 1156
Asn Ser Leu Ile Arg Arg Ser Thr Cys Ser Gly Leu Lys Asp Val Cys
365 370 375

gaa ctg gga agc ttg agg agt tcc att ata tac cca cag aag tca aat 1204
Glu Leu Gly Ser Leu Arg Ser Ser Ile Ile Tyr Pro Gln Lys Ser Asn
380 385 390 395

aac tca gga ttt ggt tgg cga gat gga gac tct gat gac ctt tgt cag 1252
Asn Ser Gly Phe Gly Trp Arg Asp Gly Asp Ser Asp Asp Leu Cys Gln
400 405 410

acc gat atg gat gat ctc tgc aac att gaa tca gtc aga aac aat gtt 1300
Thr Asp Met Asp Asp Leu Cys Asn Ile Glu Ser Val Arg Asn Asn Val
415 420 425

ttg tca cag tcc acc gat tta aac aag agt ttt aat ccc atg tgt gat 1348
Leu Ser Gln Ser Thr Asp Leu Asn Lys Ser Phe Asn Pro Met Cys Asp
430 435 440

tcc acg gat aac tgg tct tgc aag ttt gat gaa agc cca aaa gtg atg 1396
Ser Thr Asp Asn Trp Ser Cys Lys Phe Asp Glu Ser Pro Lys Val Met
445 450 455

aaa agc aaa tct aac ctg ctt tct tac caa gct tct caa ctc caa act 1444
Lys Ser Lys Ser Asn Leu Leu Ser Tyr Gln Ala Ser Gln Leu Gln Thr
460 465 470 475

gga gtt cca tgt gat gag gaa acc agc tta aca ttt gct ggt ggc tct 1492
Gly Val Pro Cys Asp Glu Glu Thr Ser Leu Thr Phe Ala Gly Gly Ser
480 485 490

tcc gtt gca gag gat gat tat aaa ggc aca gag ttg aaa ata aaa tca 1540
Ser Val Ala Glu Asp Asp Tyr Lys Gly Thr Glu Leu Lys Ile Lys Ser
495 500 505

ttt ttg gat gag aag gct cag gat ttg aaa agg ttg cag acc cct ctg 1588
Phe Leu Asp Glu Lys Ala Gln Asp Leu Lys Arg Leu Gln Thr Pro Leu
510 515 520

ctt gaa gaa ttc cac aat gct atg aat cca gga ata ccc caa ggt gca 1636
Leu Glu Glu Phe His Asn Ala Met Asn Pro Gly Ile Pro Gln Gly Ala
525 530 535

ctt gga gac acc aat atc tac aat tta cca aac tta cca agt ata agc 1684
Leu Gly Asp Thr Asn Ile Tyr Asn Leu Pro Asn Leu Pro Ser Ile Ser
540 545 550 555

aag aca cct aaa cga ctt ccg agt aga cga ctc tca gca atc agt gat 1732
Lys Thr Pro Lys Arg Leu Pro Ser Arg Arg Leu Ser Ala Ile Ser Asp
560 565 570

gct atg ccc agc cca ctc aaa agc tcc aaa cgt aca ctg aac aca agc 1780
Ala Met Pro Ser Pro Leu Lys Ser Ser Lys Arg Thr Leu Asn Thr Ser
575 580 585

aga gtg atg cag tca gga act gaa cca act caa gtc aac gag tcg acc 1828
Arg Val Met Gln Ser Gly Thr Glu Pro Thr Gln Val Asn Glu Ser Thr
590 595 600

aag aag gga gta aat aat agc cgt tgt ttc tca gag ata cgt cgg aag 1876
Lys Lys Gly Val Asn Asn Ser Arg Cys Phe Ser Glu Ile Arg Arg Lys
605 610 615

tgg gaa gaa gaa ctc tat gaa gag ctt gag agg cat cga gag aat ctg 1924
Trp Glu Glu Glu Leu Tyr Glu Glu Leu Glu Arg His Arg Glu Asn Leu
620 625 630 635

cga cac gct ggt gca gga ggg aag act cca tta tca ggc cac aaa gga 1972
Arg His Ala Gly Ala Gly Gly Lys Thr Pro Leu Ser Gly His Lys Gly
640 645 650

tag tgaacggct 1984

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<213> Arabidopsis thaliana

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20 25 30

Val Gly Lys Ile Asn Ser Ser Ile Arg Ser Ser Arg Ile Gly Leu Phe
35 40 45

Ser Lys Pro Pro Pro Gly Leu Pro Ala Pro Arg Lys Glu Glu Ala Pro
50 55 60

Ser Ile Arg Trp Arg Lys Gly Glu Leu Ile Gly Cys Gly Ala Phe Gly
65 70 75 80

Arg Val Tyr Met Gly Met Asn Leu Asp Ser Gly Glu Leu Leu Ala Ile
85 90 95

Lys Gln Val Leu Ile Ala Pro Ser Ser Ala Ser Lys Glu Lys Thr Gln
100 105 110

Gly His Ile Arg Glu Leu Glu Glu Glu Val Gln Leu Leu Lys Asn Leu
115 120 125

Ser His Pro Asn Ile Val Arg Tyr Leu Gly Thr Val Arg Glu Ser Asp
130 135 140

Ser Leu Asn Ile Leu Met Glu Phe Val Pro Gly Gly Ser Ile Ser Ser
145 150 155 160

Leu Leu Glu Lys Phe Gly Ser Phe Pro Glu Pro Val Ile Ile Met Tyr
165 170 175

Thr Lys Gln Leu Leu Leu Gly Leu Glu Tyr Leu His Asn Asn Gly Ile
180 185 190

Met His Arg Asp Ile Lys Gly Ala Asn Ile Leu Val Asp Asn Lys Gly
195 200 205

Cys Ile Arg Leu Ala Asp Phe Gly Ala Ser Lys Lys Val Val Glu Leu
210 215 220

Ala Thr Val Asn Gly Ala Lys Ser Met Lys Gly Thr Pro Tyr Trp Met
225 230 235 240

Ala Pro Glu Val Ile Leu Gln Thr Gly His Ser Phe Ser Ala Asp Ile
245 250 255

Trp Ser Val Gly Cys Thr Val Ile Glu Met Ala Thr Gly Lys Pro Pro
260 265 270

Trp Ser Glu Gln Tyr Gln Gln Phe Ala Ala Val Leu His Ile Gly Arg
275 280 285

Thr Lys Ala His Pro Pro Ile Pro Glu Asp Leu Ser Pro Glu Ala Lys
290 295 300

Asp Phe Leu Met Lys Cys Leu His Lys Glu Pro Ser Leu Arg Leu Ser
305 310 315 320

Ala Thr Glu Leu Leu Gln His Pro Phe Val Thr Gly Lys Arg Gln Glu
325 330 335

Pro Tyr Pro Ala Tyr Arg Asn Ser Leu Thr Glu Cys Gly Asn Pro Ile
340 345 350

Thr Thr Gln Gly Met Asn Val Arg Ser Ser Ile Asn Ser Leu Ile Arg
355 360 365

Arg Ser Thr Cys Ser Gly Leu Lys Asp Val Cys Glu Leu Gly Ser Leu
370 375 380

Arg Ser Ser Ile Ile Tyr Pro Gln Lys Ser Asn Asn Ser Gly Phe Gly
385 390 395 400

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Trp Arg Asp Gly Asp Ser Asp Asp Leu Cys Gln Thr Asp Met Asp Asp
                405                 410                 415

Leu Cys Asn Ile Glu Ser Val Arg Asn Asn Val Leu Ser Gln Ser Thr
            420                 425                 430

Asp Leu Asn Lys Ser Phe Asn Pro Met Cys Asp Ser Thr Asp Asn Trp
        435                 440                 445

Ser Cys Lys Phe Asp Glu Ser Pro Lys Val Met Lys Ser Lys Ser Asn
    450                 455                 460

Leu Leu Ser Tyr Gln Ala Ser Gln Leu Gln Thr Gly Val Pro Cys Asp
465                 470                 475                 480

Glu Glu Thr Ser Leu Thr Phe Ala Gly Gly Ser Ser Val Ala Glu Asp
                485                 490                 495

Asp Tyr Lys Gly Thr Glu Leu Lys Ile Lys Ser Phe Leu Asp Glu Lys
            500                 505                 510

Ala Gln Asp Leu Lys Arg Leu Gln Thr Pro Leu Leu Glu Glu Phe His
        515                 520                 525

Asn Ala Met Asn Pro Gly Ile Pro Gln Gly Ala Leu Gly Asp Thr Asn
    530                 535                 540

Ile Tyr Asn Leu Pro Asn Leu Pro Ser Ile Ser Lys Thr Pro Lys Arg
545                 550                 555                 560

Leu Pro Ser Arg Arg Leu Ser Ala Ile Ser Asp Ala Met Pro Ser Pro
                565                 570                 575

Leu Lys Ser Ser Lys Arg Thr Leu Asn Thr Ser Arg Val Met Gln Ser
            580                 585                 590

Gly Thr Glu Pro Thr Gln Val Asn Glu Ser Thr Lys Lys Gly Val Asn
        595                 600                 605

Asn Ser Arg Cys Phe Ser Glu Ile Arg Arg Lys Trp Glu Glu Glu Leu
    610                 615                 620

Tyr Glu Glu Leu Glu Arg His Arg Glu Asn Leu Arg His Ala Gly Ala
625                 630                 635                 640

Gly Gly Lys Thr Pro Leu Ser Gly His Lys Gly
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<220>
<221> CDS

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Met Pro Pro Pro Lys Met Leu Pro Pro Thr Ala Arg Asp Ser Val Ala
1 5 10 15

ggg aca ggg ggt agt cca cca cct cca cct cca cca cca gct cgg tgg 96
Gly Thr Gly Gly Ser Pro Pro Pro Pro Pro Pro Pro Pro Ala Arg Trp
20 25 30

agg gta gcg ggg gag gga gga ttg gat aca aca cca ccg ccg ccc cct 144
Arg Val Ala Gly Glu Gly Gly Leu Asp Thr Thr Pro Pro Pro Pro Pro
35 40 45

cca acg gca gat aca gtc gtg gcg gga agg acg agt tta ggt gag gcg 192
Pro Thr Ala Asp Thr Val Val Ala Gly Arg Thr Ser Leu Gly Glu Ala
50 55 60

ccc cct cct cgt cag cct cca cgt cct cca aca gca cgg tgg tca gcg 240
Pro Pro Pro Arg Gln Pro Pro Arg Pro Pro Thr Ala Arg Trp Ser Ala
65 70 75 80

atg ggc aga gtg atg tgc agt ccg ccg ata cca cta tcg cgg agt aga 288
Met Gly Arg Val Met Cys Ser Pro Pro Ile Pro Leu Ser Arg Ser Arg
85 90 95

cta gcg ctt gac gac caa cgt tgg ccg gat tgg aca acg aac ggt tgg 336
Leu Ala Leu Asp Asp Gln Arg Trp Pro Asp Trp Thr Thr Asn Gly Trp
100 105 110

cta agc atg aga ccg acg tcc tcg cca aca agg cga att gac cca caa 384
Leu Ser Met Arg Pro Thr Ser Ser Pro Thr Arg Arg Ile Asp Pro Gln
115 120 125

ggg gcc cga cga tcc tca gtg tca cca gcg ccg gtg aca acg ggg atg 432
Gly Ala Arg Arg Ser Ser Val Ser Pro Ala Pro Val Thr Thr Gly Met
130 135 140

gcc acc tct cgc act gac gat acg cta ata gag gca gag acc ggt cgc 480
Ala Thr Ser Arg Thr Asp Asp Thr Leu Ile Glu Ala Glu Thr Gly Arg
145 150 155 160

gac tgg acg agg aaa cga atg gtc agg aaa ttg ctt aaa gca agg gcg 528
Asp Trp Thr Arg Lys Arg Met Val Arg Lys Leu Leu Lys Ala Arg Ala
165 170 175

aaa gac tac aag gag ggg gga att gcg gca tac ttt ggt tta cga gtg 576
Lys Asp Tyr Lys Glu Gly Gly Ile Ala Ala Tyr Phe Gly Leu Arg Val
180 185 190

ctg cga tgc tac tcg agg atc gta cga tcg atg aaa cgc cca ggc aac 624
Leu Arg Cys Tyr Ser Arg Ile Val Arg Ser Met Lys Arg Pro Gly Asn
195 200 205

ttg aaa ttc acg tgc cgg agg gat gtg gca ata gcc acg ttc agc ggc 672
Leu Lys Phe Thr Cys Arg Arg Asp Val Ala Ile Ala Thr Phe Ser Gly

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    210                 215                 220

aca ggc aga atg cag ctg agt atg aac agc cgt ttg cga gtc gag agc    720
Thr Gly Arg Met Gln Leu Ser Met Asn Ser Arg Leu Arg Val Glu Ser
225                 230                 235                 240

ctc gtg tcc gcg ggc cag agc gtg gcg tca ttc tgc ctt ttc ctg ata    768
Leu Val Ser Ala Gly Gln Ser Val Ala Ser Phe Cys Leu Phe Leu Ile
                245                 250                 255

tgc acg gcg ccc tcg gcg atg cgg ctg gtt agc ctt ctt aca ctg acc    816
Cys Thr Ala Pro Ser Ala Met Arg Leu Val Ser Leu Leu Thr Leu Thr
            260                 265                 270

cca agc atg acc tac cta aca tgc ggg ctg gga tgg atg acc gtc gtc    864
Pro Ser Met Thr Tyr Leu Thr Cys Gly Leu Gly Trp Met Thr Val Val
        275                 280                 285

gta ctg ccg gcg ata gtg gtc cac tgt tat atg cgc cga cat acg gaa    912
Val Leu Pro Ala Ile Val Val His Cys Tyr Met Arg Arg His Thr Glu
    290                 295                 300

ggg gga tgg cgg tat gcg gca ctc gag gag cat aag acg gag ccg gga    960
Gly Gly Trp Arg Tyr Ala Ala Leu Glu Glu His Lys Thr Glu Pro Gly
305                 310                 315                 320

cga aat gaa aag atc acc cgg agt aga cgc aac tcg gcg ttc ggc ggg    1008
Arg Asn Glu Lys Ile Thr Arg Ser Arg Arg Asn Ser Ala Phe Gly Gly
                325                 330                 335

ctg gtc ggt cga aat aaa aga cga aag aag tcc aag gtc tcc ggg gca    1056
Leu Val Gly Arg Asn Lys Arg Arg Lys Lys Ser Lys Val Ser Gly Ala
            340                 345                 350

ccg aca gcg gtt tac aca gcg atg ttt ttc atg ttc tcc acg gca atc    1104
Pro Thr Ala Val Tyr Thr Ala Met Phe Phe Met Phe Ser Thr Ala Ile
        355                 360                 365

aag ggg atg gtg gtg tgc aca atg aaa aaa aaa gtc aaa aaa agt gcg    1152
Lys Gly Met Val Val Cys Thr Met Lys Lys Lys Val Lys Lys Ser Ala
    370                 375                 380

aat cgc aga ctc cgc cag ttg ctc cga tgg gcg cga tac cac gcg aac    1200
Asn Arg Arg Leu Arg Gln Leu Leu Arg Trp Ala Arg Tyr His Ala Asn
385                 390                 395                 400

gcg ttc ttg ctc tgt tct ctt gca tgc gca cga ttc gcg gca tcg cga    1248
Ala Phe Leu Leu Cys Ser Leu Ala Cys Ala Arg Phe Ala Ala Ser Arg
                405                 410                 415

acg gtc atc cat tgc agt att tac cca cgt ttc ggc ccc tta gcc acg    1296
Thr Val Ile His Cys Ser Ile Tyr Pro Arg Phe Gly Pro Leu Ala Thr
            420                 425                 430

gtg acg gcc ata tgt ttg ata cta cac acg tgt acg tac cga cgt acg    1344
Val Thr Ala Ile Cys Leu Ile Leu His Thr Cys Thr Tyr Arg Arg Thr
        435                 440                 445
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gag gca gac acg acg cga cac gaa aat gac gac gcc cgg aag gtg atg 1392
Glu Ala Asp Thr Thr Arg His Glu Asn Asp Asp Ala Arg Lys Val Met
450 455 460

gaa gac atg gcc aaa cga atg gac gat agt agc agt ggg agc acg ttg 1440
Glu Asp Met Ala Lys Arg Met Asp Asp Ser Ser Ser Gly Ser Thr Leu
465 470 475 480

agc acg ctc acg act gac gag acg tac cac acc acc acg gag gtg acc 1488
Ser Thr Leu Thr Thr Asp Glu Thr Tyr His Thr Thr Thr Glu Val Thr
485 490 495

gat ttt gat tca tct cca tcg tgg gga cga tgc tca tcg cgg cgc ccg 1536
Asp Phe Asp Ser Ser Pro Ser Trp Gly Arg Cys Ser Ser Arg Arg Pro
500 505 510

ccg gcg ctg ctg gaa tcg aca ttt cgg cga tcc ccg aga ggg tcg acg 1584
Pro Ala Leu Leu Glu Ser Thr Phe Arg Arg Ser Pro Arg Gly Ser Thr
515 520 525

gga cga cga tgg cga gag tag attcggagtc aggaacgttg gaccgacagg 1635
Gly Arg Arg Trp Arg Glu
530 535

tggaccggtt tagggcagtt gacggtaggg gttgcctgac cagccttgac gctcgacagc 1695

taaaaaaaac caacaaaaaa aaaaaaaaac aaaaaaaaaa a 1736

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<213> Arabidopsis thaliana

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Gly Thr Gly Gly Ser Pro Pro Pro Pro Pro Pro Pro Pro Ala Arg Trp
20 25 30

Arg Val Ala Gly Glu Gly Gly Leu Asp Thr Thr Pro Pro Pro Pro Pro
35 40 45

Pro Thr Ala Asp Thr Val Val Ala Gly Arg Thr Ser Leu Gly Glu Ala
50 55 60

Pro Pro Pro Arg Gln Pro Pro Arg Pro Pro Thr Ala Arg Trp Ser Ala
65 70 75 80

Met Gly Arg Val Met Cys Ser Pro Pro Ile Pro Leu Ser Arg Ser Arg
85 90 95

Leu Ala Leu Asp Asp Gln Arg Trp Pro Asp Trp Thr Thr Asn Gly Trp
100 105 110

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Leu Ser Met Arg Pro Thr Ser Ser Pro Thr Arg Arg Ile Asp Pro Gln
        115                 120                 125

Gly Ala Arg Arg Ser Ser Val Ser Pro Ala Pro Val Thr Thr Gly Met
    130                 135                 140

Ala Thr Ser Arg Thr Asp Asp Thr Leu Ile Glu Ala Glu Thr Gly Arg
145                 150                 155                 160

Asp Trp Thr Arg Lys Arg Met Val Arg Lys Leu Leu Lys Ala Arg Ala
                165                 170                 175

Lys Asp Tyr Lys Glu Gly Gly Ile Ala Ala Tyr Phe Gly Leu Arg Val
            180                 185                 190

Leu Arg Cys Tyr Ser Arg Ile Val Arg Ser Met Lys Arg Pro Gly Asn
        195                 200                 205

Leu Lys Phe Thr Cys Arg Arg Asp Val Ala Ile Ala Thr Phe Ser Gly
    210                 215                 220

Thr Gly Arg Met Gln Leu Ser Met Asn Ser Arg Leu Arg Val Glu Ser
225                 230                 235                 240

Leu Val Ser Ala Gly Gln Ser Val Ala Ser Phe Cys Leu Phe Leu Ile
                245                 250                 255

Cys Thr Ala Pro Ser Ala Met Arg Leu Val Ser Leu Leu Thr Leu Thr
            260                 265                 270

Pro Ser Met Thr Tyr Leu Thr Cys Gly Leu Gly Trp Met Thr Val Val
        275                 280                 285

Val Leu Pro Ala Ile Val Val His Cys Tyr Met Arg Arg His Thr Glu
    290                 295                 300

Gly Gly Trp Arg Tyr Ala Ala Leu Glu Glu His Lys Thr Glu Pro Gly
305                 310                 315                 320

Arg Asn Glu Lys Ile Thr Arg Ser Arg Arg Asn Ser Ala Phe Gly Gly
                325                 330                 335

Leu Val Gly Arg Asn Lys Arg Arg Lys Lys Ser Lys Val Ser Gly Ala
            340                 345                 350

Pro Thr Ala Val Tyr Thr Ala Met Phe Phe Met Phe Ser Thr Ala Ile
        355                 360                 365

Lys Gly Met Val Val Cys Thr Met Lys Lys Lys Val Lys Lys Ser Ala
    370                 375                 380

Asn Arg Arg Leu Arg Gln Leu Leu Arg Trp Ala Arg Tyr His Ala Asn
385                 390                 395                 400

Ala Phe Leu Leu Cys Ser Leu Ala Cys Ala Arg Phe Ala Ala Ser Arg
                405                 410                 415
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Thr Val Ile His Cys Ser Ile Tyr Pro Arg Phe Gly Pro Leu Ala Thr
420 425 430

Val Thr Ala Ile Cys Leu Ile Leu His Thr Cys Thr Tyr Arg Arg Thr
435 440 445

Glu Ala Asp Thr Thr Arg His Glu Asn Asp Asp Ala Arg Lys Val Met
450 455 460

Glu Asp Met Ala Lys Arg Met Asp Asp Ser Ser Ser Gly Ser Thr Leu
465 470 475 480

Ser Thr Leu Thr Thr Asp Glu Thr Tyr His Thr Thr Thr Glu Val Thr
485 490 495

Asp Phe Asp Ser Ser Pro Ser Trp Gly Arg Cys Ser Ser Arg Arg Pro
500 505 510

Pro Ala Leu Leu Glu Ser Thr Phe Arg Arg Ser Pro Arg Gly Ser Thr
515 520 525

Gly Arg Arg Trp Arg Glu
530

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<213> Arabidopsis thaliana

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<222> (18)..(77)

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<222> (156)..(314)

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Ala Lys Lys Gly Ala Asn Leu Phe Lys
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ccgctgaaaa ttctcacggc gcattctatc ccgcagaact tttctgacca ctttgtag 155

acc cgc tgc gct cag tgc cac acc ctg aag gcc ggc gag ggc aac aag 203
Thr Arg Cys Ala Gln Cys His Thr Leu Lys Ala Gly Glu Gly Asn Lys
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att ggc cct gag ctc cac ggt ctc ttc ggc cgc aag act ggt tcc gtc    251
Ile Gly Pro Glu Leu His Gly Leu Phe Gly Arg Lys Thr Gly Ser Val
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gct ggc tac tca tac acc gac gcc aac aag cag aag ggt atc gag tgg    299
Ala Gly Tyr Ser Tyr Thr Asp Ala Asn Lys Gln Lys Gly Ile Glu Trp
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aag gac gac act ctc gtacgtcacg ccaccggaag attgaaatgt ccccgagacc    354
Lys Asp Asp Thr Leu
    70

ctccgctaac acgacacag ttc gag tac ctc gag aac ccc aag aag tac att   406
                     Phe Glu Tyr Leu Glu Asn Pro Lys Lys Tyr Ile
                         75                  80

ccc ggt acc aag atg gcc ttc ggt ggt ctc aag aag ccc aag gac cgc    454
Pro Gly Thr Lys Met Ala Phe Gly Gly Leu Lys Lys Pro Lys Asp Arg
85                  90                  95                  100

aac gac ctc atc acc ttc ctt gag gag gag acc aaa taa gcgtcttgct     503
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Glu Gly Asn Lys Ile Gly Pro Glu Leu His Gly Leu Phe Gly Arg Lys
        35                  40                  45

Thr Gly Ser Val Ala Gly Tyr Ser Tyr Thr Asp Ala Asn Lys Gln Lys
    50                  55                  60

Gly Ile Glu Trp Lys Asp Asp Thr Leu Phe Glu Tyr Leu Glu Asn Pro
65                  70                  75                  80

Lys Lys Tyr Ile Pro Gly Thr Lys Met Ala Phe Gly Gly Leu Lys Lys
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tta atc aga act cca caa aca aaa caa cgt ctc aat ttc cac tca aaa    96
Leu Ile Arg Thr Pro Gln Thr Lys Gln Arg Leu Asn Phe His Ser Lys
             20                  25                  30

acc cca aac cca gac gga tct aaa gat cca tct cca ccg gag cat cca   144
Thr Pro Asn Pro Asp Gly Ser Lys Asp Pro Ser Pro Pro Glu His Pro
         35                  40                  45
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gtt gaa gta atc ggc cgg atc cga gat tac cct gac cgg aaa gag aaa    192
Val Glu Val Ile Gly Arg Ile Arg Asp Tyr Pro Asp Arg Lys Glu Lys
     50                  55                  60

tca cct tcg atc tta caa gtc aac aca gat aat caa acg gta cga gtc    240
Ser Pro Ser Ile Leu Gln Val Asn Thr Asp Asn Gln Thr Val Arg Val
 65                  70                  75                  80

aga gct gat gtt ggg tac aga gac ttc aca ctc gac ggt gtt tct ttc    288
Arg Ala Asp Val Gly Tyr Arg Asp Phe Thr Leu Asp Gly Val Ser Phe
                 85                  90                  95

tcg gag caa gaa ggt ctt gaa gag ttc tac aag aag ttt ata gaa gag    336
Ser Glu Gln Glu Gly Leu Glu Glu Phe Tyr Lys Lys Phe Ile Glu Glu
            100                 105                 110

agg att aaa gga gtg aaa gtt ggg aat aaa tgc acg att atg atg tat    384
Arg Ile Lys Gly Val Lys Val Gly Asn Lys Cys Thr Ile Met Met Tyr
        115                 120                 125

gga cct act ggt gct gga aag agt cat act atg ttt ggt tgt ggg aaa    432
Gly Pro Thr Gly Ala Gly Lys Ser His Thr Met Phe Gly Cys Gly Lys
    130                 135                 140

gag cct ggg att gtg tat cgt tct ttg aga gat ata ttg gga gat tct    480
Glu Pro Gly Ile Val Tyr Arg Ser Leu Arg Asp Ile Leu Gly Asp Ser
145                 150                 155                 160

gat caa gat ggt gtt act ttt gtt caa gtt act gtt ctt gag gtt tat    528
Asp Gln Asp Gly Val Thr Phe Val Gln Val Thr Val Leu Glu Val Tyr
                165                 170                 175

aat gag gag att tat gat ctt ctt tcg act aat agt agt aac aat tta    576
Asn Glu Glu Ile Tyr Asp Leu Leu Ser Thr Asn Ser Ser Asn Asn Leu
            180                 185                 190

ggt att ggt tgg cct aaa gga gca agc act aag gtaaagtttc ttgattgata 629
Gly Ile Gly Trp Pro Lys Gly Ala Ser Thr Lys
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actttagtat acattgaatt ggctttaaag gtgtgtactt tgttgttttg ttacag gtg 688
                                                              Val

agg ctt gaa gta atg ggg aaa aag gcg aaa aac gca agt ttt att tct    736
Arg Leu Glu Val Met Gly Lys Lys Ala Lys Asn Ala Ser Phe Ile Ser
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ggg aca gag gct ggg aag att tct aaa gaa att gtc aaa gtg gag aaa    784
Gly Thr Glu Ala Gly Lys Ile Ser Lys Glu Ile Val Lys Val Glu Lys
                225                 230                 235

cgg aga att gtg aag agt aca ctt tgt aac gaa aga agt tct cgg agt    832
Arg Arg Ile Val Lys Ser Thr Leu Cys Asn Glu Arg Ser Ser Arg Ser
            240                 245                 250

cac tgc att gtaagaacga tcttcttgat tgatgtgtat gcatagcttt            881
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His Cys Ile
        255

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                                                          Ile Ile

ctt gat gtg cca act gtt ggg gga aga ttg atg ctt gtt gac atg gct   986
Leu Asp Val Pro Thr Val Gly Gly Arg Leu Met Leu Val Asp Met Ala
        260                 265                 270

ggt tct gaa aat ata gac caa gct ggg cag act gga ttt gaa gct aag   1034
Gly Ser Glu Asn Ile Asp Gln Ala Gly Gln Thr Gly Phe Glu Ala Lys
    275                 280                 285

atg caa gtaatgtttc ctctctcaat ttgtttgatt ctactaaagt tattgtagtt    1090
Met Gln
290

atggatatca actgacttat atctctcatt attcaacag act gct aag atc aac    1144
                                          Thr Ala Lys Ile Asn
                                                      295

cag gga aat att gca ctg aag cga gtt gtg gaa tct ata gca aat gga   1192
Gln Gly Asn Ile Ala Leu Lys Arg Val Val Glu Ser Ile Ala Asn Gly
            300                 305                 310

gat tct cat gta ccc ttt aga gac agc aag ctg acc atg ctt ctc cag   1240
Asp Ser His Val Pro Phe Arg Asp Ser Lys Leu Thr Met Leu Leu Gln
        315                 320                 325

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cttgaagata tttagtgttg tttctattct ctgaatgcag gac tct ttt gaa gat   1355
                                           Asp Ser Phe Glu Asp
                                                   330

gac aag tca aag att cta atg atc ctg tgt gcg agc ccg gat cca aag   1403
Asp Lys Ser Lys Ile Leu Met Ile Leu Cys Ala Ser Pro Asp Pro Lys
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gaa atg cac aag act ctc tgt act cta gag tat ggg gca aaa gca aag   1451
Glu Met His Lys Thr Leu Cys Thr Leu Glu Tyr Gly Ala Lys Ala Lys
350                 355                 360                 365

tgc ata gtt cgt ggg tct cat act cca aac aaa gat aag tat ggg ggt   1499
Cys Ile Val Arg Gly Ser His Thr Pro Asn Lys Asp Lys Tyr Gly Gly
                370                 375                 380

gat gag tct gct tct gct gtg att ttg gga tca aga ata gct gcc atg   1547
Asp Glu Ser Ala Ser Ala Val Ile Leu Gly Ser Arg Ile Ala Ala Met
            385                 390                 395

gat gag ttc att atc aaa ctc cag tct gag aag aag caa aaa gaa aaa   1595
Asp Glu Phe Ile Ile Lys Leu Gln Ser Glu Lys Lys Gln Lys Glu Lys
        400                 405                 410

gaa agg aat gag gca caa aag cag ctg aag aag aag gaa gag gaa gtt   1643
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415 420 425

gct gct tta aga tct ctt tta aca cag agg gaa gct tgt gct acc aat 1691
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430 435 440 445

gaa gag gag ata aaa gag aaa gta aac gag aga acc cag ctt ttg aag 1739
Glu Glu Glu Ile Lys Glu Lys Val Asn Glu Arg Thr Gln Leu Leu Lys
450 455 460

tcg gaa cta gat aag aaa ctt gaa gaa tgc cga aga atg gct gag gaa 1787
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465 470 475

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Phe Val Glu Met Glu Arg Arg Arg Met Glu Glu Arg Ile Val Gln Gln
480 485 490

caa gag gaa ctg gag atg atg agg aga cgg tta gag gaa atc gag gtt 1883
Gln Glu Glu Leu Glu Met Met Arg Arg Arg Leu Glu Glu Ile Glu Val
495 500 505

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Glu Phe Arg Arg Ser Asn Gly Gly Ser Val Asp Glu Thr Ser Gly Phe
510 515 520 525

gcc aaa aga ctc agg agt ctt tac tct gat gat gat cct ggt atg gtg 1979
Ala Lys Arg Leu Arg Ser Leu Tyr Ser Asp Asp Asp Pro Gly Met Val
530 535 540

aag tca atg gac ctt gac atg ggt gat cca gaa cct gtc aag caa gtg 2027
Lys Ser Met Asp Leu Asp Met Gly Asp Pro Glu Pro Val Lys Gln Val
545 550 555

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Trp Gly Ala Val Ser His Gln Ser Ser Asn Thr Ile Ser Ser Asn Phe
560 565 570

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Thr Asn Leu Leu Gln Pro Lys Pro Ser Glu Asn Met Leu Thr Gln Met
575 580 585

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Tyr Pro Asp Arg Val Cys Leu Ser Thr Val Phe Glu Glu Glu Glu Val
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Ile Thr Thr Pro Met Pro Ser Leu Asn Ser Glu Gly Leu Gly Lys Glu
625 630 635

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Ser Gln His Ser Gly Gln Glu Glu Asp Gln Ala Asn Ile Ala Ser Pro
670 675 680 685

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795 800

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850 855 860

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925

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930 935

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Val Glu Val Ile Gly Arg Ile Arg Asp Tyr Pro Asp Arg Lys Glu Lys

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Asp Gln Asp Gly Val Thr Phe Val Gln Val Thr Val Leu Glu Val Tyr
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Gly Lys Ile Ser Lys Glu Ile Val Lys Val Glu Lys Arg Arg Ile Val
225                 230                 235                 240

Lys Ser Thr Leu Cys Asn Glu Arg Ser Ser Arg Ser His Cys Ile Ile
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Ser Lys Leu Thr Met Leu Leu Gln Asp Ser Phe Glu Asp Asp Lys Ser
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Lys Thr Leu Cys Thr Leu Glu Tyr Gly Ala Lys Ala Lys Cys Ile Val
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Asp Lys Lys Leu Glu Glu Cys Arg Arg Met Ala Glu Glu Phe Val Glu
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565 570 575

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580 585 590

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595 600 605

Glu Glu Lys Val Ile Val Glu Asp Lys Ser Ile Cys Leu Ile Thr Thr
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Glu Lys Glu Ser Thr Val Gln Ala Thr Ser Leu Pro Leu Cys Asn Gly
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His Ala Tyr Leu Ala Thr Leu Arg Pro Gly Lys Ser Ser Gln His Lys
820 825 830

Ser Leu Gln Pro Ala Ser Pro Leu Pro Leu Asn Pro Ile Glu Asn Met
835 840 845

Met Glu Val Thr Pro Ile Ser Lys Val Thr Pro Asn His Gln Ile Leu
850 855 860

Leu Lys Thr Glu Thr Glu Arg Leu Gly Glu Ala Asp Tyr Ile Asn Ser
865 870 875 880

Leu Ser Leu Ser His Phe Leu Ile Leu Phe Pro Arg Gly Glu Ser His
885 890 895

Gln His Arg Met Leu Ser Phe His Ser His Gln Thr Ser Pro Ser Leu
900 905 910

Ser Ser Phe Pro Leu Leu Ser Arg Ala Asp Ala Asp Glu Pro Gly Leu
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ggtttgatta acgttttgca tcggag atg ggt ttg gtc atg agg ttt gat ctt 173
Met Gly Leu Val Met Arg Phe Asp Leu
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tac ctt atg ttt gtg atg ttg atg ggt tta ggg ttt acg ata tca aat 221
Tyr Leu Met Phe Val Met Leu Met Gly Leu Gly Phe Thr Ile Ser Asn
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Gly Tyr Lys Phe Tyr Val Gly Gly Lys Asp Gly Trp Val Pro Thr Pro

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Ser Glu Asp Tyr Ser His Trp Ser His Arg Asn Arg Phe Gln Val Asn
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gac act ctt c gtaagtctat ttcctcttct ctactatata tacacaatgt         367
Asp Thr Leu H
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gtcaatatta atgcatagta attttgattt ttacaag at ttt aag tac gcc aag    421
                                         is Phe Lys Tyr Ala Lys
                                                        65

gga aaa gat tca gtg ttg gag gtg act gaa caa gag tac aac aca tgc    469
Gly Lys Asp Ser Val Leu Glu Val Thr Glu Gln Glu Tyr Asn Thr Cys
            70                  75                  80

aac acg aca cac ccc ctg act tcc ctc tca gac gga gac tct ctc ttc    517
Asn Thr Thr His Pro Leu Thr Ser Leu Ser Asp Gly Asp Ser Leu Phe
        85                  90                  95

cta ctt agc cac tca ggt tcc tac ttt ttc att agt ggc aac tct caa    565
Leu Leu Ser His Ser Gly Ser Tyr Phe Phe Ile Ser Gly Asn Ser Gln
    100                 105                 110

aac tgt ctt aaa ggt cag aag cta gcc gtc aag gtc ttg tcc acc gtc    613
Asn Cys Leu Lys Gly Gln Lys Leu Ala Val Lys Val Leu Ser Thr Val
115                 120                 125                 130

cac cac agc cac tct cct cgt cat acc tct ccc tcc ccg tct ccg gtc    661
His His Ser His Ser Pro Arg His Thr Ser Pro Ser Pro Ser Pro Val
                135                 140                 145

cat cag gag ttg tct tcg ccg ggg cct tct cca gga gtg gaa cca tca    709
His Gln Glu Leu Ser Ser Pro Gly Pro Ser Pro Gly Val Glu Pro Ser
            150                 155                 160

tct gat tca aac tct cgt gtt cca gct cca gga ccg gct aca gct ccc    757
Ser Asp Ser Asn Ser Arg Val Pro Ala Pro Gly Pro Ala Thr Ala Pro
        165                 170                 175

aat tcg gcc ggt ttg gtt ggt ccg ggg atg gtg gtt ctt gtgattatga     806
Asn Ser Ala Gly Leu Val Gly Pro Gly Met Val Val Leu
    180                 185                 190

taagttctct gttttgaggg gtttatatat tgtcgctagt cattaaattt gtgagggtat 866

taattactct accattgagt ttcatattta tgtgcctttt tatttgtatg tttgaagcat 926

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cacactaata tgaatatata cgacgaatat gtagagttca catagctcat gcaataaaac 1106

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gatcgaaccc acggcctcgt gggtaaaagc cacgcgctct accactgagc taagacggct 1346

atatgacaaa aaatttaaat tatgttaatt attgtatgtt tttgcagatc aaattaccaa 1406

tgaaatagtt ggtatttag gtt gtt aac tca atc ata aag ccg att gac tct  1458
                    Val Val Asn Ser Ile Ile Lys Pro Ile Asp Ser
                                195                 200

ttt ttg ttg aag agc ttg cct ctt gtt gtg gat gtg gct gtt           1500
Phe Leu Leu Lys Ser Leu Pro Leu Val Val Asp Val Ala Val
        205                 210                 215

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      Gly Ile Ser Thr Ser Arg Gln Leu Gln Ala Ser Glu Glu Pro Val
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Ser Ser Pro Leu Ser Ser Pro Ala Leu Leu Gly Ser Gly Lys Glu Glu
            235                 240                 245

gag cag aag att atc cca aag cgt cag aaa gtt cag gct gtc ctc aag   3626
Glu Gln Lys Ile Ile Pro Lys Arg Gln Lys Val Gln Ala Val Leu Lys
        250                 255                 260

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Ser Ile Lys Gln
    265

gatctgctcc atttcgttta atatttttcc atctcaatct agttatataa tgtgcccaac 3738

cttgcttgtt ttcag agt cct aag aag gtc aac ctg gtt gca gca cta gtc 3789
                 Ser Pro Lys Lys Val Asn Leu Val Ala Ala Leu Val
                         270                 275

cgt ggc atg cgt gtt gaa gat gct ttg atc caa ttg cag gtc aca gtc   3837
Arg Gly Met Arg Val Glu Asp Ala Leu Ile Gln Leu Gln Val Thr Val
280                 285                 290                 295

aaa cga gct gca caa act gtg tac cgg gtaatctctg agatccgagt        3884
Lys Arg Ala Ala Gln Thr Val Tyr Arg
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                            Val Ile His Ala Ala Arg Ala Asn Ala
                            305                 310

act cat aac cat gga cta gat cct gac cgt ctc ctt gtt g gtatgtaaaa 4106
Thr His Asn His Gly Leu Asp Pro Asp Arg Leu Leu Val A
    315                 320                 325

ctgattctgg atccctgatt tccttgtttt acatttaaaa agagaacgtg atatttttaga 4166

gagttcgccg attggtactt taaggaagca aacatgatat gccagaacga tgtatttcat 4226

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                            la Glu Ala Phe Val Gly Lys Gly Leu
                                       330                 335

ttt ggg aag aag gta gct tac cat gca aaa gga aga agc ggg att ata  4325
Phe Gly Lys Lys Val Ala Tyr His Ala Lys Gly Arg Ser Gly Ile Ile
                340                 345                 350

tca ata ccc cgg tgt cgc cta aca gtc ata gtt aga gag acg act cca  4373
Ser Ile Pro Arg Cys Arg Leu Thr Val Ile Val Arg Glu Thr Thr Pro
            355                 360                 365

gag gaa gaa gct gag att gca agg ctc aaa gtt cac aat ttt aag aag  4421
Glu Glu Glu Ala Glu Ile Ala Arg Leu Lys Val His Asn Phe Lys Lys
        370                 375                 380

aaa agc aaa cgg gag aga cag ctt gta cca cac aag ctc atc gag aca  4469
Lys Ser Lys Arg Glu Arg Gln Leu Val Pro His Lys Leu Ile Glu Thr
    385                 390                 395

agt cca ata tgg aac cgc aga ggt acc aaa gcc aat cat cgg tcc tca  4517
Ser Pro Ile Trp Asn Arg Arg Gly Thr Lys Ala Asn His Arg Ser Ser
400                 405                 410                 415

gag ttg gtacggtcgt ctcactagta tctttgttcc cgcaattgca acaagagctt  4573
Glu Leu

ctctgttatg gtaaattgct tttttttttg gttttggttt gatattgtat tggaactcta 4633

taggacctgt ttgcttcttg tattcaataa acatgttccc agagaggaaa cttcacttaa 4693

caaaagcgtc tctgtttttc tccattctgt ttctggag gtg tta aca atc att ttg 4749
                                          Val Leu Thr Ile Ile Leu
                                                  420

gat gta act tgt gtt gga aac atg gaa aaa aat cgt ctg gat aat ttg  4797
Asp Val Thr Cys Val Gly Asn Met Glu Lys Asn Arg Leu Asp Asn Leu
    425                 430                 435

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Thr Asn Gln Asn Asn Ile Tyr His His Asn Pro Glu G
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gctgacccat taaactcgat ccacgcctga taattctcgc cactgttaag cttcagctcc 6704

gtgaatctct ggccgtctct gcctccatag aa acc tgc agt ttc aga tgc aac   6757
                                  lu Thr Cys Ser Phe Arg Cys Asn
                                                 455

gga agt gag aga att gac gtc gac gcc gac gtg gtt gtc gtt gat gtc   6805
Gly Ser Glu Arg Ile Asp Val Asp Ala Asp Val Val Val Val Asp Val
460                 465                 470                 475

gtt gaa ctc ttg gtt agc gaa aac atc gaa ttc aac ggc gaa gat tcg   6853
Val Glu Leu Leu Val Ser Glu Asn Ile Glu Phe Asn Gly Glu Asp Ser
                480                 485                 490

gct att ggg gtc acc gtt att ggt gaa gtt gaa gag gcc gag atg ctg   6901
Ala Ile Gly Val Thr Val Ile Gly Glu Val Glu Glu Ala Glu Met Leu
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Arg

ggc                                                               6960


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             20                  25                  30

Gly Lys Asp Gly Trp Val Pro Thr Pro Ser Glu Asp Tyr Ser His Trp
         35                  40                  45

Ser His Arg Asn Arg Phe Gln Val Asn Asp Thr Leu His Phe Lys Tyr
    50                  55                  60

Ala Lys Gly Lys Asp Ser Val Leu Glu Val Thr Glu Gln Glu Tyr Asn
 65                  70                  75                  80

Thr Cys Asn Thr Thr His Pro Leu Thr Ser Leu Ser Asp Gly Asp Ser
                 85                  90                  95

Leu Phe Leu Leu Ser His Ser Gly Ser Tyr Phe Phe Ile Ser Gly Asn
            100                 105                 110

Ser Gln Asn Cys Leu Lys Gly Gln Lys Leu Ala Val Lys Val Leu Ser
        115                 120                 125
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Thr Val His His Ser His Ser Pro Arg His Thr Ser Pro Ser Pro Ser
    130                 135                 140

Pro Val His Gln Glu Leu Ser Ser Pro Gly Pro Ser Pro Gly Val Glu
145                 150                 155                 160

Pro Ser Ser Asp Ser Asn Ser Arg Val Pro Ala Pro Gly Pro Ala Thr
                165                 170                 175

Ala Pro Asn Ser Ala Gly Leu Val Gly Pro Gly Met Val Val Leu Val
            180                 185                 190

Val Asn Ser Ile Ile Lys Pro Ile Asp Ser Phe Leu Leu Lys Ser Leu
        195                 200                 205

Pro Leu Val Val Asp Val Ala Val Gly Ile Ser Thr Ser Arg Gln Leu
    210                 215                 220

Gln Ala Ser Glu Glu Pro Val Ser Ser Pro Leu Ser Ser Pro Ala Leu
225                 230                 235                 240

Leu Gly Ser Gly Lys Glu Glu Glu Gln Lys Ile Ile Pro Lys Arg Gln
                245                 250                 255

Lys Val Gln Ala Val Leu Lys Ser Ile Lys Gln Ser Pro Lys Lys Val
            260                 265                 270

Asn Leu Val Ala Ala Leu Val Arg Gly Met Arg Val Glu Asp Ala Leu
        275                 280                 285

Ile Gln Leu Gln Val Thr Val Lys Arg Ala Ala Gln Thr Val Tyr Arg
    290                 295                 300

Val Ile His Ala Ala Arg Ala Asn Ala Thr His Asn His Gly Leu Asp
305                 310                 315                 320

Pro Asp Arg Leu Leu Val Ala Glu Ala Phe Val Gly Lys Gly Leu Phe
                325                 330                 335

Gly Lys Lys Val Ala Tyr His Ala Lys Gly Arg Ser Gly Ile Ile Ser
            340                 345                 350

Ile Pro Arg Cys Arg Leu Thr Val Ile Val Arg Glu Thr Thr Pro Glu
        355                 360                 365

Glu Glu Ala Glu Ile Ala Arg Leu Lys Val His Asn Phe Lys Lys Lys
    370                 375                 380

Ser Lys Arg Glu Arg Gln Leu Val Pro His Lys Leu Ile Glu Thr Ser
385                 390                 395                 400

Pro Ile Trp Asn Arg Arg Gly Thr Lys Ala Asn His Arg Ser Ser Glu
                405                 410                 415

Leu Val Leu Thr Ile Ile Leu Asp Val Thr Cys Val Gly Asn Met Glu
            420                 425                 430
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Lys Asn Arg Leu Asp Asn Leu Thr Asn Gln Asn Asn Ile Tyr His His
        435                 440                 445

Asn Pro Glu Glu Thr Cys Ser Phe Arg Cys Asn Gly Ser Glu Arg Ile
    450                 455                 460

Asp Val Asp Ala Asp Val Val Val Val Asp Val Val Glu Leu Leu Val
465                 470                 475                 480

Ser Glu Asn Ile Glu Phe Asn Gly Glu Asp Ser Ala Ile Gly Val Thr
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Val Ile Gly Glu Val Glu Glu Ala Glu Met Leu Arg
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                            1               5

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Tyr Ala Ala Thr Cys Leu Ser Val Glu Asp Ala Val Asn Ala Arg Ser
 10                  15                  20                  25

ata agc aat tgc aat gtc ctc gca ttc tcc ggc atc aaa aca tcc ccg     148
Ile Ser Asn Cys Asn Val Leu Ala Phe Ser Gly Ile Lys Thr Ser Pro
                 30                  35                  40

gaa acc gcc ttg gaa atc ttc gac gct tgg atc aaa act cct ttc aaa     196
Glu Thr Ala Leu Glu Ile Phe Asp Ala Trp Ile Lys Thr Pro Phe Lys
             45                  50                  55

tct cct tgt cct gcg tcc gga tcc gaa cca tgg agc tca gtt atc tct     244
Ser Pro Cys Pro Ala Ser Gly Ser Glu Pro Trp Ser Ser Val Ile Ser
         60                  65                  70

tcc ttc ctc gac aat tct ctc tcc gag atg tct cag att gga aag tca     292
Ser Phe Leu Asp Asn Ser Leu Ser Glu Met Ser Gln Ile Gly Lys Ser
     75                  80                  85

acc gcc ggc gat tca aca acc aag aag atc gat gaa aca acc gcg tct     340
Thr Ala Gly Asp Ser Thr Thr Lys Lys Ile Asp Glu Thr Thr Ala Ser
 90                  95                 100                 105

tgc gta att tgc tgc ttg gcg aag aac aga gag ttc act cca gtg gac     388
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Cys Val Ile Cys Cys Leu Ala Lys Asn Arg Glu Phe Thr Pro Val Asp
                110                 115                 120

atc atg ccg gga ggc tcg atg aag atc gtt aga gag acg ccg acg tcg     436
Ile Met Pro Gly Gly Ser Met Lys Ile Val Arg Glu Thr Pro Thr Ser
            125                 130                 135

gcg att gta aga ttc aaa gcg gga agt gtg gaa ccg gcg cat cac cac     484
Ala Ile Val Arg Phe Lys Ala Gly Ser Val Glu Pro Ala His His His
        140                 145                 150

aca ttc ggc cat gac ctt gta gtc ata aag gga aag aaa agt gtg tgg     532
Thr Phe Gly His Asp Leu Val Val Ile Lys Gly Lys Lys Ser Val Trp
    155                 160                 165

aat ctg agc aag aag gag aga gct gat ctc gtt gac ggc gat tac cta     580
Asn Leu Ser Lys Lys Glu Arg Ala Asp Leu Val Asp Gly Asp Tyr Leu
170                 175                 180                 185

ttc act ccc gcc ggt gat gtt cac cga gtc aaa tat cac gaa gac act     628
Phe Thr Pro Ala Gly Asp Val His Arg Val Lys Tyr His Glu Asp Thr
                190                 195                 200

gag ttc ttc atc act tgg gat ggc cat tgg gac ata ttc ctt gac gaa     676
Glu Phe Phe Ile Thr Trp Asp Gly His Trp Asp Ile Phe Leu Asp Glu
            205                 210                 215

gac ctc gaa act gca aag aaa gcc atc gaa gaa gaa gct tga             718
Asp Leu Glu Thr Ala Lys Lys Ala Ile Glu Glu Glu Ala
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Ala Phe Ser Gly Ile Lys Thr Ser Pro Glu Thr Ala Leu Glu Ile Phe
         35                  40                  45

Asp Ala Trp Ile Lys Thr Pro Phe Lys Ser Pro Cys Pro Ala Ser Gly
     50                  55                  60

Ser Glu Pro Trp Ser Ser Val Ile Ser Ser Phe Leu Asp Asn Ser Leu
 65                  70                  75                  80

Ser Glu Met Ser Gln Ile Gly Lys Ser Thr Ala Gly Asp Ser Thr Thr
                 85                  90                  95
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Lys Lys Ile Asp Glu Thr Thr Ala Ser Cys Val Ile Cys Cys Leu Ala
            100                 105                 110

Lys Asn Arg Glu Phe Thr Pro Val Asp Ile Met Pro Gly Gly Ser Met
        115                 120                 125

Lys Ile Val Arg Glu Thr Pro Thr Ser Ala Ile Val Arg Phe Lys Ala
    130                 135                 140

Gly Ser Val Glu Pro Ala His His His Thr Phe Gly His Asp Leu Val
145                 150                 155                 160

Val Ile Lys Gly Lys Lys Ser Val Trp Asn Leu Ser Lys Lys Glu Arg
                165                 170                 175

Ala Asp Leu Val Asp Gly Asp Tyr Leu Phe Thr Pro Ala Gly Asp Val
            180                 185                 190

His Arg Val Lys Tyr His Glu Asp Thr Glu Phe Phe Ile Thr Trp Asp
        195                 200                 205

Gly His Trp Asp Ile Phe Leu Asp Glu Asp Leu Glu Thr Ala Lys Lys
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Ala Ile Glu Glu Glu Ala
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             Met Thr Ile Arg Asn Gln Arg Phe Ser Leu Leu Lys Gln
             1               5                   10

cct ata tcc tcc aca ctt aat cag cat tta gta gat tat cca acc ccg   98
Pro Ile Ser Ser Thr Leu Asn Gln His Leu Val Asp Tyr Pro Thr Pro
    15                  20                  25

agc aat ctt agt tat tgg tgg ggg ttc ggt ccg tta gct ggt att tgt   146
Ser Asn Leu Ser Tyr Trp Trp Gly Phe Gly Pro Leu Ala Gly Ile Cys
30                  35                  40                  45

tta gtc att cag ata gtg act ggc gtt ttt tta gct atg cat tac aca   194
Leu Val Ile Gln Ile Val Thr Gly Val Phe Leu Ala Met His Tyr Thr
                50                  55                  60

cct cat gtg gat tta gct ttc aac agc gta gaa cac att atg aga gat   242
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```
Pro His Val Asp Leu Ala Phe Asn Ser Val Glu His Ile Met Arg Asp
            65                  70                  75

gtt gaa ggg ggc tgg ttg ctc cgt tat atg cat gct aat ggg gca agt      290
Val Glu Gly Gly Trp Leu Leu Arg Tyr Met His Ala Asn Gly Ala Ser
        80                  85                  90

atg ttt ctt att gtg gtt tac ctt cat att ttt cgt ggt cta tat cat      338
Met Phe Leu Ile Val Val Tyr Leu His Ile Phe Arg Gly Leu Tyr His
    95                  100                 105

gcg agt tat agc agt cct agg gaa ttt gtt tgg tgt ctt gga gtt gta      386
Ala Ser Tyr Ser Ser Pro Arg Glu Phe Val Trp Cys Leu Gly Val Val
110                 115                 120                 125

atc ttc cta tta atg att gtg aca gct ttt ata gga tat gta cta cct      434
Ile Phe Leu Leu Met Ile Val Thr Ala Phe Ile Gly Tyr Val Leu Pro
                130                 135                 140

tgg ggt cag atg agc ttt tgg gga gct aca gta att aca agc tta gct      482
Trp Gly Gln Met Ser Phe Trp Gly Ala Thr Val Ile Thr Ser Leu Ala
            145                 150                 155

agc gcc ata cct gta gta gga gat acc ata gtg act tgg ctt tgg ggt      530
Ser Ala Ile Pro Val Val Gly Asp Thr Ile Val Thr Trp Leu Trp Gly
        160                 165                 170

ggt ttc tcc gtg gac aat gcc acc tta aat cgt ttt ttt agt ctt cat      578
Gly Phe Ser Val Asp Asn Ala Thr Leu Asn Arg Phe Phe Ser Leu His
    175                 180                 185

cat tta ctc ccc ttt att tta gta ggc gcc agt ctt ctt cat ctg gcc      626
His Leu Leu Pro Phe Ile Leu Val Gly Ala Ser Leu Leu His Leu Ala
190                 195                 200                 205

gca ttg cat caa tat gga tca aat aat cca ttg ggt gta cat tct gag      674
Ala Leu His Gln Tyr Gly Ser Asn Asn Pro Leu Gly Val His Ser Glu
                210                 215                 220

atg gat aaa ata gct ttt tac cct tat ttt tat gtc aag gat cta gtt      722
Met Asp Lys Ile Ala Phe Tyr Pro Tyr Phe Tyr Val Lys Asp Leu Val
            225                 230                 235

ggt tgg gta gct ttt gct atc ttt ttt tct att tgg att ttt tat gct      770
Gly Trp Val Ala Phe Ala Ile Phe Phe Ser Ile Trp Ile Phe Tyr Ala
        240                 245                 250

cct aat gtt ttg gga cat ccc gac aat tat ata cct gct aat ccg atg      818
Pro Asn Val Leu Gly His Pro Asp Asn Tyr Ile Pro Ala Asn Pro Met
    255                 260                 265

tcc acc ccg cct cat att gtg ccg gaa tgg tat ttc cta ccg atc cat      866
Ser Thr Pro Pro His Ile Val Pro Glu Trp Tyr Phe Leu Pro Ile His
270                 275                 280                 285

gcc att ctt cgt agt ata cct gac aaa gcg gga ggt gta gcc gca ata      914
Ala Ile Leu Arg Ser Ile Pro Asp Lys Ala Gly Gly Val Ala Ala Ile
```

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                    290                 295                 300

gca cca gtt ttt ata tgt ctc ttg gct tta cct ttt ttt aaa agt atg    962
Ala Pro Val Phe Ile Cys Leu Leu Ala Leu Pro Phe Phe Lys Ser Met
            305                 310                 315

tat gtg cgt agt tca agt ttt cga ccg att cac caa gga atg ttt tgg   1010
Tyr Val Arg Ser Ser Ser Phe Arg Pro Ile His Gln Gly Met Phe Trp
        320                 325                 330

ttg ctt ttg gcg gat tgc tta cta cta ggt tgg atc gga tgt caa cct   1058
Leu Leu Leu Ala Asp Cys Leu Leu Leu Gly Trp Ile Gly Cys Gln Pro
    335                 340                 345

gtg gag gct cca ttt gtt act att gga caa att tct cct ttg gtt ttc   1106
Val Glu Ala Pro Phe Val Thr Ile Gly Gln Ile Ser Pro Leu Val Phe
350                 355                 360                 365

ttc ttg ttc ttt gcc ata acg ccc att ctg gga cga gtt gga aga gga   1154
Phe Leu Phe Phe Ala Ile Thr Pro Ile Leu Gly Arg Val Gly Arg Gly
                370                 375                 380

att cct aat tct tac acg gat gag act gat cac acc tga tcagtgaaaa    1203
Ile Pro Asn Ser Tyr Thr Asp Glu Thr Asp His Thr
            385                 390


<210> 46
<211> 393
<212> PRT
<213> Arabidopsis thaliana

<400> 46
Met Thr Ile Arg Asn Gln Arg Phe Ser Leu Leu Lys Gln Pro Ile Ser
 1               5                  10                  15

Ser Thr Leu Asn Gln His Leu Val Asp Tyr Pro Thr Pro Ser Asn Leu
            20                  25                  30

Ser Tyr Trp Trp Gly Phe Gly Pro Leu Ala Gly Ile Cys Leu Val Ile
        35                  40                  45

Gln Ile Val Thr Gly Val Phe Leu Ala Met His Tyr Thr Pro His Val
    50                  55                  60

Asp Leu Ala Phe Asn Ser Val Glu His Ile Met Arg Asp Val Glu Gly
65                  70                  75                  80

Gly Trp Leu Leu Arg Tyr Met His Ala Asn Gly Ala Ser Met Phe Leu
                85                  90                  95

Ile Val Val Tyr Leu His Ile Phe Arg Gly Leu Tyr His Ala Ser Tyr
            100                 105                 110

Ser Ser Pro Arg Glu Phe Val Trp Cys Leu Gly Val Val Ile Phe Leu
        115                 120                 125
```

```
Leu Met Ile Val Thr Ala Phe Ile Gly Tyr Val Leu Pro Trp Gly Gln
    130                 135                 140

Met Ser Phe Trp Gly Ala Thr Val Ile Thr Ser Leu Ala Ser Ala Ile
145                 150                 155                 160

Pro Val Val Gly Asp Thr Ile Val Thr Trp Leu Trp Gly Gly Phe Ser
                165                 170                 175

Val Asp Asn Ala Thr Leu Asn Arg Phe Phe Ser Leu His His Leu Leu
            180                 185                 190

Pro Phe Ile Leu Val Gly Ala Ser Leu Leu His Leu Ala Ala Leu His
        195                 200                 205

Gln Tyr Gly Ser Asn Asn Pro Leu Gly Val His Ser Glu Met Asp Lys
    210                 215                 220

Ile Ala Phe Tyr Pro Tyr Phe Tyr Val Lys Asp Leu Val Gly Trp Val
225                 230                 235                 240

Ala Phe Ala Ile Phe Phe Ser Ile Trp Ile Phe Tyr Ala Pro Asn Val
                245                 250                 255

Leu Gly His Pro Asp Asn Tyr Ile Pro Ala Asn Pro Met Ser Thr Pro
            260                 265                 270

Pro His Ile Val Pro Glu Trp Tyr Phe Leu Pro Ile His Ala Ile Leu
        275                 280                 285

Arg Ser Ile Pro Asp Lys Ala Gly Gly Val Ala Ala Ile Ala Pro Val
    290                 295                 300

Phe Ile Cys Leu Leu Ala Leu Pro Phe Phe Lys Ser Met Tyr Val Arg
305                 310                 315                 320

Ser Ser Ser Phe Arg Pro Ile His Gln Gly Met Phe Trp Leu Leu Leu
                325                 330                 335

Ala Asp Cys Leu Leu Leu Gly Trp Ile Gly Cys Gln Pro Val Glu Ala
            340                 345                 350

Pro Phe Val Thr Ile Gly Gln Ile Ser Pro Leu Val Phe Phe Leu Phe
        355                 360                 365

Phe Ala Ile Thr Pro Ile Leu Gly Arg Val Gly Arg Gly Ile Pro Asn
    370                 375                 380

Ser Tyr Thr Asp Glu Thr Asp His Thr
385                 390
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<210> 47
<211> 1194
<212> DNA
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<220>
<221> CDS
<222> (1)..(1194)

<400> 47
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Met Arg Lys Val Ser Ser Val Ile Ser Val Val Asp Pro Val Ile Phe
  1               5                  10                  15

cga gga aat tac gca gct aca ctc gat gtg tcg tat ccg gta ttc ccg      96
Arg Gly Asn Tyr Ala Ala Thr Leu Asp Val Ser Tyr Pro Val Phe Pro
             20                  25                  30

caa aat aaa gat ggc cgt gca ctt cag aaa gtt ctc gga acc att cgt     144
Gln Asn Lys Asp Gly Arg Ala Leu Gln Lys Val Leu Gly Thr Ile Arg
         35                  40                  45

aac gga gat ttg gct gtt tcg gct cct aaa aca agt ctt agg gca ggt     192
Asn Gly Asp Leu Ala Val Ser Ala Pro Lys Thr Ser Leu Arg Ala Gly
     50                  55                  60

att ttc ggt gaa ggt tcc agc ttg gtc gat cag atg ccc tgt aaa gtt     240
Ile Phe Gly Glu Gly Ser Ser Leu Val Asp Gln Met Pro Cys Lys Val
 65                  70                  75                  80

tac gtg gcg ttc cac aaa gaa tca tac tgc tcg ctt acc ggg cta agc     288
Tyr Val Ala Phe His Lys Glu Ser Tyr Cys Ser Leu Thr Gly Leu Ser
                 85                  90                  95

aaa cgc gga gtc gca ata aac gaa gca agt ctt tcc ctg gtc gga atc     336
Lys Arg Gly Val Ala Ile Asn Glu Ala Ser Leu Ser Leu Val Gly Ile
            100                 105                 110

act aaa gtt aga gcc ccc gtc gga aat acc gtt gga gcg gaa gca acc     384
Thr Lys Val Arg Ala Pro Val Gly Asn Thr Val Gly Ala Glu Ala Thr
        115                 120                 125

gta tac ata ggt agt cca aaa cct tat aca gag tgt agt act cca aat     432
Val Tyr Ile Gly Ser Pro Lys Pro Tyr Thr Glu Cys Ser Thr Pro Asn
    130                 135                 140

aaa atg tat gcg gtt gca gct ggt ttc aag gtg gca agt ttc gcc gct     480
Lys Met Tyr Ala Val Ala Ala Gly Phe Lys Val Ala Ser Phe Ala Ala
145                 150                 155                 160

agt acg tgc gta cgt ccg cct gca cgt gca cgt cgt acg ctg acc gtg     528
Ser Thr Cys Val Arg Pro Pro Ala Arg Ala Arg Arg Thr Leu Thr Val
                165                 170                 175

acg tcg acc gtg acg ctg tct atg gca act ggt aaa tgc gta aat aca     576
Thr Ser Thr Val Thr Leu Ser Met Ala Thr Gly Lys Cys Val Asn Thr
            180                 185                 190

gga aac gaa cca gta tct aaa cct aca gga gta cgt atg atg tta att     624
Gly Asn Glu Pro Val Ser Lys Pro Thr Gly Val Arg Met Met Leu Ile
        195                 200                 205
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cct ctc gat gct act ctc att aaa gta tgg act ggg gaa gta aaa aaa     672
Pro Leu Asp Ala Thr Leu Ile Lys Val Trp Thr Gly Glu Val Lys Lys
    210                 215                 220

gcg ata gtt tcc cgg cct gca aaa att ttc aat agc gta gga aat tta     720
Ala Ile Val Ser Arg Pro Ala Lys Ile Phe Asn Ser Val Gly Asn Leu
225                 230                 235                 240

gaa cgt cct tca att tcg cat tct tgt gga caa ggt ttg gat gaa gct     768
Glu Arg Pro Ser Ile Ser His Ser Cys Gly Gln Gly Leu Asp Glu Ala
                245                 250                 255

gcc gct tat atc aag ggt aga ctt tct cca atc gtt aaa gca gaa aga     816
Ala Ala Tyr Ile Lys Gly Arg Leu Ser Pro Ile Val Lys Ala Glu Arg
            260                 265                 270

att aaa gtt ttg gtt aaa gac gag cac gaa gaa gta aaa gaa ctt ctt     864
Ile Lys Val Leu Val Lys Asp Glu His Glu Glu Val Lys Glu Leu Leu
        275                 280                 285

caa gaa ggt tac gaa gaa atc gtc ggt gag tct cca agt ttc aat tta     912
Gln Glu Gly Tyr Glu Glu Ile Val Gly Glu Ser Pro Ser Phe Asn Leu
    290                 295                 300

gca caa gaa gcg tgg gaa aaa gct gaa aga cga gca aaa ggt cag tcc     960
Ala Gln Glu Ala Trp Glu Lys Ala Glu Arg Arg Ala Lys Gly Gln Ser
305                 310                 315                 320

ccg tgc agt gcg gca aaa gca aac ctt gca acc tac tat ttt tca aca     1008
Pro Cys Ser Ala Ala Lys Ala Asn Leu Ala Thr Tyr Tyr Phe Ser Thr
                325                 330                 335

ggt gat ttc gaa aaa tca att aaa ctc tac gaa gaa cct atg ggt ttg     1056
Gly Asp Phe Glu Lys Ser Ile Lys Leu Tyr Glu Glu Pro Met Gly Leu
            340                 345                 350

aaa gat act gat aag agc tat ctg cga gaa cgt aga aaa aga gta gag     1104
Lys Asp Thr Asp Lys Ser Tyr Leu Arg Glu Arg Arg Lys Arg Val Glu
        355                 360                 365

gct act acg ttg cgt gca ccg ttc gtg gtc cag ctg acc gtg cgt agt     1152
Ala Thr Thr Leu Arg Ala Pro Phe Val Val Gln Leu Thr Val Arg Ser
    370                 375                 380

cgt acg acg atg atc gcc gtt ggt gaa agc aac gca aac tga             1194
Arg Thr Thr Met Ile Ala Val Gly Glu Ser Asn Ala Asn
385                 390                 395
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<210> 48
<211> 397
<212> PRT
<213> Arabidopsis thaliana

<400> 48

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Met Arg Lys Val Ser Ser Val Ile Ser Val Val Asp Pro Val Ile Phe
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1               5                   10                  15
Arg Gly Asn Tyr Ala Ala Thr Leu Asp Val Ser Tyr Pro Val Phe Pro
            20                  25                  30
Gln Asn Lys Asp Gly Arg Ala Leu Gln Lys Val Leu Gly Thr Ile Arg
        35                  40                  45
Asn Gly Asp Leu Ala Val Ser Ala Pro Lys Thr Ser Leu Arg Ala Gly
    50                  55                  60
Ile Phe Gly Glu Gly Ser Ser Leu Val Asp Gln Met Pro Cys Lys Val
65                  70                  75                  80
Tyr Val Ala Phe His Lys Glu Ser Tyr Cys Ser Leu Thr Gly Leu Ser
                85                  90                  95
Lys Arg Gly Val Ala Ile Asn Glu Ala Ser Leu Ser Leu Val Gly Ile
            100                 105                 110
Thr Lys Val Arg Ala Pro Val Gly Asn Thr Val Gly Ala Glu Ala Thr
        115                 120                 125
Val Tyr Ile Gly Ser Pro Lys Pro Tyr Thr Glu Cys Ser Thr Pro Asn
    130                 135                 140
Lys Met Tyr Ala Val Ala Ala Gly Phe Lys Val Ala Ser Phe Ala Ala
145                 150                 155                 160
Ser Thr Cys Val Arg Pro Pro Ala Arg Ala Arg Arg Thr Leu Thr Val
                165                 170                 175
Thr Ser Thr Val Thr Leu Ser Met Ala Thr Gly Lys Cys Val Asn Thr
            180                 185                 190
Gly Asn Glu Pro Val Ser Lys Pro Thr Gly Val Arg Met Met Leu Ile
        195                 200                 205
Pro Leu Asp Ala Thr Leu Ile Lys Val Trp Thr Gly Glu Val Lys Lys
    210                 215                 220
Ala Ile Val Ser Arg Pro Ala Lys Ile Phe Asn Ser Val Gly Asn Leu
225                 230                 235                 240
Glu Arg Pro Ser Ile Ser His Ser Cys Gly Gln Gly Leu Asp Glu Ala
                245                 250                 255
Ala Ala Tyr Ile Lys Gly Arg Leu Ser Pro Ile Val Lys Ala Glu Arg
            260                 265                 270
Ile Lys Val Leu Val Lys Asp Glu His Glu Glu Val Lys Glu Leu Leu
        275                 280                 285
Gln Glu Gly Tyr Glu Glu Ile Val Gly Glu Ser Pro Ser Phe Asn Leu
    290                 295                 300
Ala Gln Glu Ala Trp Glu Lys Ala Glu Arg Arg Ala Lys Gly Gln Ser
```

305 310 315 320

Pro Cys Ser Ala Ala Lys Ala Asn Leu Ala Thr Tyr Tyr Phe Ser Thr
325 330 335

Gly Asp Phe Glu Lys Ser Ile Lys Leu Tyr Glu Glu Pro Met Gly Leu
340 345 350

Lys Asp Thr Asp Lys Ser Tyr Leu Arg Glu Arg Arg Lys Arg Val Glu
355 360 365

Ala Thr Thr Leu Arg Ala Pro Phe Val Val Gln Leu Thr Val Arg Ser
370 375 380

Arg Thr Thr Met Ile Ala Val Gly Glu Ser Asn Ala Asn
385 390 395

<210> 49
<211> 611
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (5)..(601)

<400> 49
gaaa atg atc gta ctt tct gtt ggt tcc gct tct tca tct ccg atc gtc 49
Met Ile Val Leu Ser Val Gly Ser Ala Ser Ser Ser Pro Ile Val
1 5 10 15

gtc gtc ttt tcc gtc gcg ctt ctt ctg ttc tac ttc tct gaa act tct 97
Val Val Phe Ser Val Ala Leu Leu Leu Phe Tyr Phe Ser Glu Thr Ser
20 25 30

cta gga gct cct tgt ccc atc aat ggc ttg cca atc gtg agg aat att 145
Leu Gly Ala Pro Cys Pro Ile Asn Gly Leu Pro Ile Val Arg Asn Ile
35 40 45

agt gac ctt cct cag gat aac tat gga aga cca ggt ctt tcc cac atg 193
Ser Asp Leu Pro Gln Asp Asn Tyr Gly Arg Pro Gly Leu Ser His Met
50 55 60

act gtt gct ggc tcc gta ttg cat gga atg aaa gag gtt gaa ata tgg 241
Thr Val Ala Gly Ser Val Leu His Gly Met Lys Glu Val Glu Ile Trp
65 70 75

ctt cag aca ttt gct cca ggt tca gag aca cca att cac agg cac tcc 289
Leu Gln Thr Phe Ala Pro Gly Ser Glu Thr Pro Ile His Arg His Ser
80 85 90 95

tgt gaa gag gtt ttt gtt gtc cta aag ggc agt ggt act ctg tat ctc 337
Cys Glu Glu Val Phe Val Val Leu Lys Gly Ser Gly Thr Leu Tyr Leu
100 105 110

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gct gaa aca cat gga aat ttc cct ggg aaa cca atc gaa ttt cca atc    385
Ala Glu Thr His Gly Asn Phe Pro Gly Lys Pro Ile Glu Phe Pro Ile
            115                 120                 125

ttt gcc aac agt aca att cat att ccg atc aat gat gct cat cag gtc    433
Phe Ala Asn Ser Thr Ile His Ile Pro Ile Asn Asp Ala His Gln Val
        130                 135                 140

aaa aac acc ggt cat gag gac ctg cag gtg ttg gtt atc ata tct cgg    481
Lys Asn Thr Gly His Glu Asp Leu Gln Val Leu Val Ile Ile Ser Arg
    145                 150                 155

ccg cct att aaa atc ttc atc tac gaa gac tgg ttt atg cca cac act    529
Pro Pro Ile Lys Ile Phe Ile Tyr Glu Asp Trp Phe Met Pro His Thr
160                 165                 170                 175

gct gca agg ctg aag ttc cct tac tat tgg gat gag caa tgc att caa    577
Ala Ala Arg Leu Lys Phe Pro Tyr Tyr Trp Asp Glu Gln Cys Ile Gln
                180                 185                 190

gaa tca caa aaa gac gag ctt taa agcaaagtcc                         611
Glu Ser Gln Lys Asp Glu Leu
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<210> 50
<211> 198
<212> PRT
<213> Arabidopsis thaliana

<400> 50
Met Ile Val Leu Ser Val Gly Ser Ala Ser Ser Ser Pro Ile Val Val
  1               5                  10                  15

Val Phe Ser Val Ala Leu Leu Leu Phe Tyr Phe Ser Glu Thr Ser Leu
             20                  25                  30

Gly Ala Pro Cys Pro Ile Asn Gly Leu Pro Ile Val Arg Asn Ile Ser
         35                  40                  45

Asp Leu Pro Gln Asp Asn Tyr Gly Arg Pro Gly Leu Ser His Met Thr
     50                  55                  60

Val Ala Gly Ser Val Leu His Gly Met Lys Glu Val Glu Ile Trp Leu
 65                  70                  75                  80

Gln Thr Phe Ala Pro Gly Ser Glu Thr Pro Ile His Arg His Ser Cys
                 85                  90                  95

Glu Glu Val Phe Val Val Leu Lys Gly Ser Gly Thr Leu Tyr Leu Ala
            100                 105                 110

Glu Thr His Gly Asn Phe Pro Gly Lys Pro Ile Glu Phe Pro Ile Phe
        115                 120                 125

Ala Asn Ser Thr Ile His Ile Pro Ile Asn Asp Ala His Gln Val Lys
    130                 135                 140
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Asn Thr Gly His Glu Asp Leu Gln Val Leu Val Ile Ile Ser Arg Pro
145 150 155 160

Pro Ile Lys Ile Phe Ile Tyr Glu Asp Trp Phe Met Pro His Thr Ala
165 170 175

Ala Arg Leu Lys Phe Pro Tyr Tyr Trp Asp Glu Gln Cys Ile Gln Glu
180 185 190

Ser Gln Lys Asp Glu Leu
195

<210> 51
<211> 1398
<212> DNA
<213> Arabidopsis thaliana

<220>
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<222> (1)..(1398)

<400> 51
atg cct cgt cgt cgt acg tgc tgt cgg cgt gaa ttc ggt ccg aca cag 48
Met Pro Arg Arg Arg Thr Cys Cys Arg Arg Glu Phe Gly Pro Thr Gln
1 5 10 15

cca tgt aga ggc gcg tca atc act gga tct cta cgt gac cgt cga ccg 96
Pro Cys Arg Gly Ala Ser Ile Thr Gly Ser Leu Arg Asp Arg Arg Pro
20 25 30

acc gct atc ctt atc gga acc ctc acc gct tta ggc ggt gga gtt aga 144
Thr Ala Ile Leu Ile Gly Thr Leu Thr Ala Leu Gly Gly Gly Val Arg
35 40 45

tgt ggc tct tgc ccc agt gtc gac cgt tgc gga cac gca agt gcc gcc 192
Cys Gly Ser Cys Pro Ser Val Asp Arg Cys Gly His Ala Ser Ala Ala
50 55 60

ata gcg cgt gat agc tgt gcc gtg ttc gca tgg aag cga ggt acg cga 240
Ile Ala Arg Asp Ser Cys Ala Val Phe Ala Trp Lys Arg Gly Thr Arg
65 70 75 80

caa gag tac tgg tgc tcg act gaa ccg acc ctt gac tgg ggc ccc ggt 288
Gln Glu Tyr Trp Cys Ser Thr Glu Pro Thr Leu Asp Trp Gly Pro Gly
85 90 95

ggt gga ccc gac ttc gat tgt gat gat ggt ggt gac gat ccg ctt ttg 336
Gly Gly Pro Asp Phe Asp Cys Asp Asp Gly Gly Asp Asp Pro Leu Leu
100 105 110

att caa gat ggc gta aaa gct gcg gag gaa tat gct aaa tct gga aaa 384
Ile Gln Asp Gly Val Lys Ala Ala Glu Glu Tyr Ala Lys Ser Gly Lys
115 120 125

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gtt cca gat cca agc tgt act gat aat gct gag ttt caa gtt gtg ctt     432
Val Pro Asp Pro Ser Cys Thr Asp Asn Ala Glu Phe Gln Val Val Leu
    130                 135                 140

att att att agg gag ggg ttg aaa act gat cct tta aaa tac act aag     480
Ile Ile Ile Arg Glu Gly Leu Lys Thr Asp Pro Leu Lys Tyr Thr Lys
145                 150                 155                 160

cga ccc agt tgc ctt gtt ggt gtt tct gag gaa act act act ggt gtt     528
Arg Pro Ser Cys Leu Val Gly Val Ser Glu Glu Thr Thr Thr Gly Val
                165                 170                 175

aag aga agt tac caa atg cag ccg aaa tgt act ttg ctt ttg cat gct     576
Lys Arg Ser Tyr Gln Met Gln Pro Lys Cys Thr Leu Leu Leu His Ala
            180                 185                 190

act gat gtt tgt gac acc gtg atc aag agc aag att gat aac ttg tac     624
Thr Asp Val Cys Asp Thr Val Ile Lys Ser Lys Ile Asp Asn Leu Tyr
        195                 200                 205

gga tgc cgc cac tca ctt tcg gat ggt ctc atg agg gct act gat gtt     672
Gly Cys Arg His Ser Leu Ser Asp Gly Leu Met Arg Ala Thr Asp Val
    210                 215                 220

cgt cgc ccc tgc aag gta gcg ctt gta ggc ggt tac gga gat gtc ttt     720
Arg Arg Pro Cys Lys Val Ala Leu Val Gly Gly Tyr Gly Asp Val Phe
225                 230                 235                 240

aag ggt tgg gtt gct gcc ttg aag caa gct ggt gca cgt gtc atc gtg     768
Lys Gly Trp Val Ala Ala Leu Lys Gln Ala Gly Ala Arg Val Ile Val
                245                 250                 255

act gag atc ccg caa atc tgt gcc gtc caa gct acc atg gaa ggt agt     816
Thr Glu Ile Pro Gln Ile Cys Ala Val Gln Ala Thr Met Glu Gly Ser
            260                 265                 270

tcg gtc ctt acc ctt gag gat gtc gtt tca gat gtt gat cgc ttc gtt     864
Ser Val Leu Thr Leu Glu Asp Val Val Ser Asp Val Asp Arg Phe Val
        275                 280                 285

acg aca acc ggt aac aag gac ctc atc atg gtt gac cac atg agg cga     912
Thr Thr Thr Gly Asn Lys Asp Leu Ile Met Val Asp His Met Arg Arg
    290                 295                 300

atg aag aac cag gcc ata gtt tgc aac att cga cgt ttc gac aat gaa     960
Met Lys Asn Gln Ala Ile Val Cys Asn Ile Arg Arg Phe Asp Asn Glu
305                 310                 315                 320

atc gac atg cgc agt ctc gag acc ttc cct gga gtg aag cgg atc aca    1008
Ile Asp Met Arg Ser Leu Glu Thr Phe Pro Gly Val Lys Arg Ile Thr
                325                 330                 335

atc aag gcc cag act gac aga tgg gtc ttt cgc gac acc aac aga ggt    1056
Ile Lys Ala Gln Thr Asp Arg Trp Val Phe Arg Asp Thr Asn Arg Gly
            340                 345                 350

atc att gtc cca gcc gag ggg cgt ctc atg acg atg gga tgc gcc act    1104
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Ile Ile Val Pro Ala Glu Gly Arg Leu Met Thr Met Gly Cys Ala Thr
        355                 360                 365

gga cac ccc agc ttc cgg acg tcc tgc tct ttc act aac caa gtc agt    1152
Gly His Pro Ser Phe Arg Thr Ser Cys Ser Phe Thr Asn Gln Val Ser
    370                 375                 380

tct cag ctc gag ttg tgg cgg gag aag agc acc ggc aag tat gag aag    1200
Ser Gln Leu Glu Leu Trp Arg Glu Lys Ser Thr Gly Lys Tyr Glu Lys
385                 390                 395                 400

aaa gtg tac gtc ttc cca aag cac ctt gag aag aag gtt gcc gcc ctt    1248
Lys Val Tyr Val Phe Pro Lys His Leu Glu Lys Lys Val Ala Ala Leu
                405                 410                 415

cat ctc gta aag ctc gga gca agg ctc act aag ctt agt cgg tgc acg    1296
His Leu Val Lys Leu Gly Ala Arg Leu Thr Lys Leu Ser Arg Cys Thr
            420                 425                 430

ttg ttg tgc acg gac gac cca gtt gaa ggt cgt aaa gag cct cct cac    1344
Leu Leu Cys Thr Asp Asp Pro Val Glu Gly Arg Lys Glu Pro Pro His
        435                 440                 445

cgt gct ggc agc cct gaa ccg tgc cag ctg cag ctg acc gtg ttc agg    1392
Arg Ala Gly Ser Pro Glu Pro Cys Gln Leu Gln Leu Thr Val Phe Arg
    450                 455                 460

tag taa                                                            1398

465


<210> 52
<211> 464
<212> PRT
<213> Arabidopsis thaliana

<400> 52
Met Pro Arg Arg Arg Thr Cys Cys Arg Arg Glu Phe Gly Pro Thr Gln
  1               5                  10                  15

Pro Cys Arg Gly Ala Ser Ile Thr Gly Ser Leu Arg Asp Arg Arg Pro
             20                  25                  30

Thr Ala Ile Leu Ile Gly Thr Leu Thr Ala Leu Gly Gly Gly Val Arg
        35                  40                  45

Cys Gly Ser Cys Pro Ser Val Asp Arg Cys Gly His Ala Ser Ala Ala
    50                  55                  60

Ile Ala Arg Asp Ser Cys Ala Val Phe Ala Trp Lys Arg Gly Thr Arg
65                  70                  75                  80

Gln Glu Tyr Trp Cys Ser Thr Glu Pro Thr Leu Asp Trp Gly Pro Gly
                85                  90                  95

Gly Gly Pro Asp Phe Asp Cys Asp Asp Gly Gly Asp Asp Pro Leu Leu
```

100 105 110

Ile Gln Asp Gly Val Lys Ala Ala Glu Glu Tyr Ala Lys Ser Gly Lys
115 120 125

Val Pro Asp Pro Ser Cys Thr Asp Asn Ala Glu Phe Gln Val Val Leu
130 135 140

Ile Ile Ile Arg Glu Gly Leu Lys Thr Asp Pro Leu Lys Tyr Thr Lys
145 150 155 160

Arg Pro Ser Cys Leu Val Gly Val Ser Glu Glu Thr Thr Thr Gly Val
165 170 175

Lys Arg Ser Tyr Gln Met Gln Pro Lys Cys Thr Leu Leu Leu His Ala
180 185 190

Thr Asp Val Cys Asp Thr Val Ile Lys Ser Lys Ile Asp Asn Leu Tyr
195 200 205

Gly Cys Arg His Ser Leu Ser Asp Gly Leu Met Arg Ala Thr Asp Val
210 215 220

Arg Arg Pro Cys Lys Val Ala Leu Val Gly Gly Tyr Gly Asp Val Phe
225 230 235 240

Lys Gly Trp Val Ala Ala Leu Lys Gln Ala Gly Ala Arg Val Ile Val
245 250 255

Thr Glu Ile Pro Gln Ile Cys Ala Val Gln Ala Thr Met Glu Gly Ser
260 265 270

Ser Val Leu Thr Leu Glu Asp Val Val Ser Asp Val Asp Arg Phe Val
275 280 285

Thr Thr Thr Gly Asn Lys Asp Leu Ile Met Val Asp His Met Arg Arg
290 295 300

Met Lys Asn Gln Ala Ile Val Cys Asn Ile Arg Arg Phe Asp Asn Glu
305 310 315 320

Ile Asp Met Arg Ser Leu Glu Thr Phe Pro Gly Val Lys Arg Ile Thr
325 330 335

Ile Lys Ala Gln Thr Asp Arg Trp Val Phe Arg Asp Thr Asn Arg Gly
340 345 350

Ile Ile Val Pro Ala Glu Gly Arg Leu Met Thr Met Gly Cys Ala Thr
355 360 365

Gly His Pro Ser Phe Arg Thr Ser Cys Ser Phe Thr Asn Gln Val Ser
370 375 380

Ser Gln Leu Glu Leu Trp Arg Glu Lys Ser Thr Gly Lys Tyr Glu Lys
385 390 395 400

Lys Val Tyr Val Phe Pro Lys His Leu Glu Lys Lys Val Ala Ala Leu

```
                405                 410                 415

His Leu Val Lys Leu Gly Ala Arg Leu Thr Lys Leu Ser Arg Cys Thr
            420                 425                 430

Leu Leu Cys Thr Asp Asp Pro Val Glu Gly Arg Lys Glu Pro Pro His
        435                 440                 445

Arg Ala Gly Ser Pro Glu Pro Cys Gln Leu Gln Leu Thr Val Phe Arg
    450                 455                 460


<210> 53
<211> 771
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)..(537)

<400> 53
atg ccg cgt aac gtt gct ggt atg tgc gtt gcg tta gaa cga gtc ttc      48
Met Pro Arg Asn Val Ala Gly Met Cys Val Ala Leu Glu Arg Val Phe
  1               5                  10                  15

gac gtc gat gaa att gtc agg tta agg aag agg ttt ttc aag ttg gac      96
Asp Val Asp Glu Ile Val Arg Leu Arg Lys Arg Phe Phe Lys Leu Asp
             20                  25                  30

aga gat tgt tca gga tca gaa ctt gga agt gag ttc atg agt ttg cct     144
Arg Asp Cys Ser Gly Ser Glu Leu Gly Ser Glu Phe Met Ser Leu Pro
         35                  40                  45

caa gtt agt tcg aac cct ctt cgg atg cgt gag atg cgt aat ttc gat     192
Gln Val Ser Ser Asn Pro Leu Arg Met Arg Glu Met Arg Asn Phe Asp
     50                  55                  60

aat gat tgc gta ggg agt gtg gat ttt atc gag ttc atc aat gga cgt     240
Asn Asp Cys Val Gly Ser Val Asp Phe Ile Glu Phe Ile Asn Gly Arg
 65                  70                  75                  80

tcc agt ttc agt act gtc ggg cag aag aat gct aaa ttg aga ttt gca     288
Ser Ser Phe Ser Thr Val Gly Gln Lys Asn Ala Lys Leu Arg Phe Ala
                 85                  90                  95

ccg att atc tat gat tgc gat aaa gat gga cct ata tca aac ggt gag     336
Pro Ile Ile Tyr Asp Cys Asp Lys Asp Gly Pro Ile Ser Asn Gly Glu
            100                 105                 110

tta ttt agg gtg ttg cgt att atg gtt cat gac aat ctg agt gat aat     384
Leu Phe Arg Val Leu Arg Ile Met Val His Asp Asn Leu Ser Asp Asn
        115                 120                 125

cag ctg cag cag cgt tgc gat tgc acg cgt agt ggc gga gat aat gac     432
Gln Leu Gln Gln Arg Cys Asp Cys Thr Arg Ser Gly Gly Asp Asn Asp
```

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    130                 135                 140

ggg gat ggt cga ggt gcg aaa aac agc ttt gag gaa ttt tac ggt cgt    480
Gly Asp Gly Arg Gly Ala Lys Asn Ser Phe Glu Glu Phe Tyr Gly Arg
145                 150                 155                 160

ttg cca gct acc gta cgt cgg cgt ccg tac cgt acg ttg gta agc ggt    528
Leu Pro Ala Thr Val Arg Arg Arg Pro Tyr Arg Thr Leu Val Ser Gly
                165                 170                 175

gat gtg taa agttcagtgc accgtgaccg tgagcctgga agcctgaacg            577
Asp Val

ctgacaagcc cttaagccaa aaaattggct gaggcctgat gccctgagat gccaaaggct 637

ttttaggctt ttagagaaaa aggctaaaaa aaaggctaga aaaaaaggct cttaggcctg 697

cttgagcctg agcctgagcc tgatcgatca aaaaaaaagg agcctttttt ttttagctaa 757

aaaaaaaaag ctaa                                                    771


<210> 54
<211> 178
<212> PRT
<213> Arabidopsis thaliana

<400> 54
Met Pro Arg Asn Val Ala Gly Met Cys Val Ala Leu Glu Arg Val Phe
  1               5                  10                  15

Asp Val Asp Glu Ile Val Arg Leu Arg Lys Arg Phe Phe Lys Leu Asp
            20                  25                  30

Arg Asp Cys Ser Gly Ser Glu Leu Gly Ser Glu Phe Met Ser Leu Pro
        35                  40                  45

Gln Val Ser Ser Asn Pro Leu Arg Met Arg Glu Met Arg Asn Phe Asp
    50                  55                  60

Asn Asp Cys Val Gly Ser Val Asp Phe Ile Glu Phe Ile Asn Gly Arg
 65                  70                  75                  80

Ser Ser Phe Ser Thr Val Gly Gln Lys Asn Ala Lys Leu Arg Phe Ala
                85                  90                  95

Pro Ile Ile Tyr Asp Cys Asp Lys Asp Gly Pro Ile Ser Asn Gly Glu
            100                 105                 110

Leu Phe Arg Val Leu Arg Ile Met Val His Asp Asn Leu Ser Asp Asn
        115                 120                 125

Gln Leu Gln Gln Arg Cys Asp Cys Thr Arg Ser Gly Gly Asp Asn Asp
    130                 135                 140

Gly Asp Gly Arg Gly Ala Lys Asn Ser Phe Glu Glu Phe Tyr Gly Arg
145                 150                 155                 160
```

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Leu Pro Ala Thr Val Arg Arg Arg Pro Tyr Arg Thr Leu Val Ser Gly
                165                 170                 175

Asp Val



<210> 55
<211> 1617
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (10)..(1557)

<400> 55
cgctacggt atg cgt acg tca aga aca gga ttt cgg atg cca ttg ggg ccc 51
          Met Arg Thr Ser Arg Thr Gly Phe Arg Met Pro Leu Gly Pro
            1               5                  10

tgg gcg gtg aac ccc tgc ttc att gct tcc tgt tcc tgt ctc ctc gtt   99
Trp Ala Val Asn Pro Cys Phe Ile Ala Ser Cys Ser Cys Leu Leu Val
 15                  20                  25                  30

ggc ttc ggc gac gca atc ttc tac gag tcg ttc gcc ggg gat ttt gat   147
Gly Phe Gly Asp Ala Ile Phe Tyr Glu Ser Phe Ala Gly Asp Phe Asp
                35                  40                  45

gca cgc tgg att tta tcc ggc tca aag tgt ctc tcg gat tcg gcc aag   195
Ala Arg Trp Ile Leu Ser Gly Ser Lys Cys Leu Ser Asp Ser Ala Lys
            50                  55                  60

aat gct ggg ttt gat gat tat gga ctt ctt gtg ggt gaa caa gcc agg   243
Asn Ala Gly Phe Asp Asp Tyr Gly Leu Leu Val Gly Glu Gln Ala Arg
        65                  70                  75

aag cct cct ata gtc aag gaa ctt gcc gag tct ctc agt cta aag gac   291
Lys Pro Pro Ile Val Lys Glu Leu Ala Glu Ser Leu Ser Leu Lys Asp
    80                  85                  90

gga aga gtt gtt ctt gag tgt gag act cgc ctt gac cat ggc atc gac   339
Gly Arg Val Val Leu Glu Cys Glu Thr Arg Leu Asp His Gly Ile Asp
 95                 100                 105                 110

tgt gga ggt ccc tgt att aga tat ctt cga acc cag gag agc gga tgg   387
Cys Gly Gly Pro Cys Ile Arg Tyr Leu Arg Thr Gln Glu Ser Gly Trp
                115                 120                 125

aaa ttt gac agc tcc acc atg ttt ggt gct gct aag tat ggc gcg agg   435
Lys Phe Asp Ser Ser Thr Met Phe Gly Ala Ala Lys Tyr Gly Ala Arg
            130                 135                 140

agg acc cag ttc ttc ggg ggc cac ccc cag aac cca aac agt ggt gag   483
Arg Thr Gln Phe Phe Gly Gly His Pro Gln Asn Pro Asn Ser Gly Glu
        145                 150                 155
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tgt gtt gac cat gat cac aac cag cgg gct tcc ctc aca tcg gac aaa     531
Cys Val Asp His Asp His Asn Gln Arg Ala Ser Leu Thr Ser Asp Lys
    160                 165                 170

gta cct cgt ttg tac act gga att ctg tcg ccc gaa aat gaa ttc cag     579
Val Pro Arg Leu Tyr Thr Gly Ile Leu Ser Pro Glu Asn Glu Phe Gln
175                 180                 185                 190

atc ttg ata gat cgg ggg ttg gag acc aag gcc aaa atc ttc cct tgt     627
Ile Leu Ile Asp Arg Gly Leu Glu Thr Lys Ala Lys Ile Phe Pro Cys
                195                 200                 205

gag gac ttt gag cct cct gtt ata cca tcc aag aga agc cct gat aat     675
Glu Asp Phe Glu Pro Pro Val Ile Pro Ser Lys Arg Ser Pro Asp Asn
            210                 215                 220

ccg tcg aag cgg act gag gac tcg gac gaa aaa gcc aaa atc cca ggc     723
Pro Ser Lys Arg Thr Glu Asp Ser Asp Glu Lys Ala Lys Ile Pro Gly
        225                 230                 235

cca agt gcc ctg aag cga cag gaa agc gat gag gat ccg aac cgg gaa     771
Pro Ser Ala Leu Lys Arg Gln Glu Ser Asp Glu Asp Pro Asn Arg Glu
    240                 245                 250

atc tta cat gaa gaa gcc ggg aga cgt tcg tcc gat gtt ggg gcc cac     819
Ile Leu His Glu Glu Ala Gly Arg Arg Ser Ser Asp Val Gly Ala His
255                 260                 265                 270

gca aaa gac cag gca cac gaa cct gag cca aaa cac tgg ggt gct gaa     867
Ala Lys Asp Gln Ala His Glu Pro Glu Pro Lys His Trp Gly Ala Glu
                275                 280                 285

aag gat ggt gaa tgc gca ccc cca aag att gaa aac gca aag cgg ggg     915
Lys Asp Gly Glu Cys Ala Pro Pro Lys Ile Glu Asn Ala Lys Arg Gly
            290                 295                 300

gcc gcc cct agt tgt ggt gta tcg gag agg caa acc aag att agt cca     963
Ala Ala Pro Ser Cys Gly Val Ser Glu Arg Gln Thr Lys Ile Ser Pro
        305                 310                 315

aat tat aag gga aaa ccc tcc gtg ggt cca aac gtt tac caa ggg att     1011
Asn Tyr Lys Gly Lys Pro Ser Val Gly Pro Asn Val Tyr Gln Gly Ile
    320                 325                 330

tgg aaa ccc cgc gag atg cta aac cct gga tcg ttc caa atc gca aaa     1059
Trp Lys Pro Arg Glu Met Leu Asn Pro Gly Ser Phe Gln Ile Ala Lys
335                 340                 345                 350

ccc gct tgt gag cct att gct ggt ata ggc atg gag att agg aag cag     1107
Pro Ala Cys Glu Pro Ile Ala Gly Ile Gly Met Glu Ile Arg Lys Gln
                355                 360                 365

ggc atc cta tta gac act gtg gtg ggg gtt agg ggg gat aca ggt gaa     1155
Gly Ile Leu Leu Asp Thr Val Val Gly Val Arg Gly Asp Thr Gly Glu
            370                 375                 380
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gaa tat ggg gaa acc ccg ttg aag acc acg tgt acc gtc gag aag cac 1203
Glu Tyr Gly Glu Thr Pro Leu Lys Thr Thr Cys Thr Val Glu Lys His
385 390 395

agt ttg cag gct caa gag gcg aga acc cgg tca gac gct ggt tca ccc 1251
Ser Leu Gln Ala Gln Glu Ala Arg Thr Arg Ser Asp Ala Gly Ser Pro
400 405 410

tac acc agg tac gta tct aaa atc ccc ggg aaa gcc gat aat ccc ttc 1299
Tyr Thr Arg Tyr Val Ser Lys Ile Pro Gly Lys Ala Asp Asn Pro Phe
415 420 425 430

tcg agc gag cac aaa tgt aag aat ttc gat ctg att gag gct gag aaa 1347
Ser Ser Glu His Lys Cys Lys Asn Phe Asp Leu Ile Glu Ala Glu Lys
435 440 445

cag tgt gcc aat gca gta atc ctg ggt gtt gtg gtt aac tcc ggt tca 1395
Gln Cys Ala Asn Ala Val Ile Leu Gly Val Val Val Asn Ser Gly Ser
450 455 460

att aac tcc gtt gtg tct tgg ggc tac aaa cct ggc acg gtg aac aag 1443
Ile Asn Ser Val Val Ser Trp Gly Tyr Lys Pro Gly Thr Val Asn Lys
465 470 475

aac caa gaa cgc aga gca ccc tcc cag cga cgt agt agc gag att gaa 1491
Asn Gln Glu Arg Arg Ala Pro Ser Gln Arg Arg Ser Ser Glu Ile Glu
480 485 490

gga acc caa gac cga cga aaa cag gat gtt ggc cga cgc caa gct gcc 1539
Gly Thr Gln Asp Arg Arg Lys Gln Asp Val Gly Arg Arg Gln Ala Ala
495 500 505 510

agc tcg ccc agg cgc tga taattaaatc cgatccgtcc tttaaccccc 1587
Ser Ser Pro Arg Arg
515

gttgttcaat accgtttttt ttttatttaa 1617

<210> 56
<211> 515
<212> PRT
<213> Arabidopsis thaliana

<400> 56
Met Arg Thr Ser Arg Thr Gly Phe Arg Met Pro Leu Gly Pro Trp Ala
1 5 10 15

Val Asn Pro Cys Phe Ile Ala Ser Cys Ser Cys Leu Leu Val Gly Phe
20 25 30

Gly Asp Ala Ile Phe Tyr Glu Ser Phe Ala Gly Asp Phe Asp Ala Arg
35 40 45

Trp Ile Leu Ser Gly Ser Lys Cys Leu Ser Asp Ser Ala Lys Asn Ala
50 55 60

Gly Phe Asp Asp Tyr Gly Leu Leu Val Gly Glu Gln Ala Arg Lys Pro
65 70 75 80

Pro Ile Val Lys Glu Leu Ala Glu Ser Leu Ser Leu Lys Asp Gly Arg
85 90 95

Val Val Leu Glu Cys Glu Thr Arg Leu Asp His Gly Ile Asp Cys Gly
100 105 110

Gly Pro Cys Ile Arg Tyr Leu Arg Thr Gln Glu Ser Gly Trp Lys Phe
115 120 125

Asp Ser Ser Thr Met Phe Gly Ala Ala Lys Tyr Gly Ala Arg Arg Thr
130 135 140

Gln Phe Phe Gly Gly His Pro Gln Asn Pro Asn Ser Gly Glu Cys Val
145 150 155 160

Asp His Asp His Asn Gln Arg Ala Ser Leu Thr Ser Asp Lys Val Pro
165 170 175

Arg Leu Tyr Thr Gly Ile Leu Ser Pro Glu Asn Glu Phe Gln Ile Leu
180 185 190

Ile Asp Arg Gly Leu Glu Thr Lys Ala Lys Ile Phe Pro Cys Glu Asp
195 200 205

Phe Glu Pro Pro Val Ile Pro Ser Lys Arg Ser Pro Asp Asn Pro Ser
210 215 220

Lys Arg Thr Glu Asp Ser Asp Glu Lys Ala Lys Ile Pro Gly Pro Ser
225 230 235 240

Ala Leu Lys Arg Gln Glu Ser Asp Glu Asp Pro Asn Arg Glu Ile Leu
245 250 255

His Glu Glu Ala Gly Arg Arg Ser Ser Asp Val Gly Ala His Ala Lys
260 265 270

Asp Gln Ala His Glu Pro Glu Pro Lys His Trp Gly Ala Glu Lys Asp
275 280 285

Gly Glu Cys Ala Pro Pro Lys Ile Glu Asn Ala Lys Arg Gly Ala Ala
290 295 300

Pro Ser Cys Gly Val Ser Glu Arg Gln Thr Lys Ile Ser Pro Asn Tyr
305 310 315 320

Lys Gly Lys Pro Ser Val Gly Pro Asn Val Tyr Gln Gly Ile Trp Lys
325 330 335

Pro Arg Glu Met Leu Asn Pro Gly Ser Phe Gln Ile Ala Lys Pro Ala
340 345 350

Cys Glu Pro Ile Ala Gly Ile Gly Met Glu Ile Arg Lys Gln Gly Ile
355 360 365

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Leu Leu Asp Thr Val Val Gly Val Arg Gly Asp Thr Gly Glu Glu Tyr
    370                 375                 380

Gly Glu Thr Pro Leu Lys Thr Thr Cys Thr Val Glu Lys His Ser Leu
385                 390                 395                 400

Gln Ala Gln Glu Ala Arg Thr Arg Ser Asp Ala Gly Ser Pro Tyr Thr
                405                 410                 415

Arg Tyr Val Ser Lys Ile Pro Gly Lys Ala Asp Asn Pro Phe Ser Ser
            420                 425                 430

Glu His Lys Cys Lys Asn Phe Asp Leu Ile Glu Ala Glu Lys Gln Cys
        435                 440                 445

Ala Asn Ala Val Ile Leu Gly Val Val Val Asn Ser Gly Ser Ile Asn
    450                 455                 460

Ser Val Val Ser Trp Gly Tyr Lys Pro Gly Thr Val Asn Lys Asn Gln
465                 470                 475                 480

Glu Arg Arg Ala Pro Ser Gln Arg Arg Ser Ser Glu Ile Glu Gly Thr
                485                 490                 495

Gln Asp Arg Arg Lys Gln Asp Val Gly Arg Arg Gln Ala Ala Ser Ser
            500                 505                 510

Pro Arg Arg
        515


<210> 57
<211> 1281
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (13)..(1266)

<400> 57
gctccgctcg ct atg agt tgg cga ccc cgg aag aac gtg ccg atg aaa aca 51
              Met Ser Trp Arg Pro Arg Lys Asn Val Pro Met Lys Thr
                1               5                  10

cgg gtg acc agg gac ggt tcg ggg ccc gga aaa acc ggt gtc aca cgc    99
Arg Val Thr Arg Asp Gly Ser Gly Pro Gly Lys Thr Gly Val Thr Arg
     15                  20                  25

ggg tcg tca ccc atg cga tgg gca tgg aag cgg tgg caa gcc gtc ggg   147
Gly Ser Ser Pro Met Arg Trp Ala Trp Lys Arg Trp Gln Ala Val Gly
 30                  35                  40                  45

gca tcg acg gcc cgc acg tgg ttc ggg aca gag aac cag aaa gga ata   195
Ala Ser Thr Ala Arg Thr Trp Phe Gly Thr Glu Asn Gln Lys Gly Ile
                 50                  55                  60
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acg aca agc acc cgc gcg cgg cgc tac gcg gtc tcg gcc aaa ttc ccg    243
Thr Thr Ser Thr Arg Ala Arg Arg Tyr Ala Val Ser Ala Lys Phe Pro
             65                  70                  75

aga tta agt aat aag ggc aaa gat tac atg cgt tgc gtc ctc caa tac    291
Arg Leu Ser Asn Lys Gly Lys Asp Tyr Met Arg Cys Val Leu Gln Tyr
         80                  85                  90

acc gtc aaa aat gaa caa aaa gtt gat tgt ggt ggc tca tat atc aag    339
Thr Val Lys Asn Glu Gln Lys Val Asp Cys Gly Gly Ser Tyr Ile Lys
     95                 100                 105

tta tta cct tcg aaa ttg cgc acg ggt gat ggt gat ggc gtg tca gaa    387
Leu Leu Pro Ser Lys Leu Arg Thr Gly Asp Gly Asp Gly Val Ser Glu
110                 115                 120                 125

tat tca att atg ttt ggt cca gat tcg aca ggt gca tca cgt act gtt    435
Tyr Ser Ile Met Phe Gly Pro Asp Ser Thr Gly Ala Ser Arg Thr Val
                130                 135                 140

cgt cga gct cgc aat tat aag ggt aaa cgg cat ttg cgg aaa aaa gaa    483
Arg Arg Ala Arg Asn Tyr Lys Gly Lys Arg His Leu Arg Lys Lys Glu
            145                 150                 155

cag aat aaa gtg gaa aca gat caa tta aca cat cag tat act acg agt    531
Gln Asn Lys Val Glu Thr Asp Gln Leu Thr His Gln Tyr Thr Thr Ser
        160                 165                 170

tgg tca cca gat tgg acc tac aac gtt cta gta gat aat aag gaa tcg    579
Trp Ser Pro Asp Trp Thr Tyr Asn Val Leu Val Asp Asn Lys Glu Ser
    175                 180                 185

caa gca ggg aac ctt gcc gac gac tgc gag tta ctt cca cag aag cga    627
Gln Ala Gly Asn Leu Ala Asp Asp Cys Glu Leu Leu Pro Gln Lys Arg
190                 195                 200                 205

atc ttc cga ccc agc tgc cga aaa caa tcc aaa cca gtc acc tgc gta    675
Ile Phe Arg Pro Ser Cys Arg Lys Gln Ser Lys Pro Val Thr Cys Val
                210                 215                 220

gac gtc aag cac cac gcc ccc cga cga aat gtg aaa ccc gcc ggg cac    723
Asp Val Lys His His Ala Pro Arg Arg Asn Val Lys Pro Ala Gly His
            225                 230                 235

gat gac att cca gcg cga cgg acg acg ccg gaa gcg gtc cgg aaa ggc    771
Asp Asp Ile Pro Ala Arg Arg Thr Thr Pro Glu Ala Val Arg Lys Gly
        240                 245                 250

cgc acg aac gag cga ccg gac cgg acg tgg gcg acc ggg acg acc cca    819
Arg Thr Asn Glu Arg Pro Asp Arg Thr Trp Ala Thr Gly Thr Thr Pro
    255                 260                 265

cgg cca cgg cgt tac aag gga gag acg aag gcc aaa aag cac cca cgg    867
Arg Pro Arg Arg Tyr Lys Gly Glu Thr Lys Ala Lys Lys His Pro Arg
270                 275                 280                 285
```

ccg gaa tac aaa ggg acc tgg gtc acg ccg tta cag gac aac ccc act 915
Pro Glu Tyr Lys Gly Thr Trp Val Thr Pro Leu Gln Asp Asn Pro Thr
290 295 300

cca gcc ccc ccg aac gac cta tat cta ttc ttg gac ctg ggt gca gca 963
Pro Ala Pro Pro Asn Asp Leu Tyr Leu Phe Leu Asp Leu Gly Ala Ala
305 310 315

ggg aca cgg acc tgg acc gtg aaa tcg ggc tca atc acg aac aac atg 1011
Gly Thr Arg Thr Trp Thr Val Lys Ser Gly Ser Ile Thr Asn Asn Met
320 325 330

ata gtg aca acg tcc gtg gaa acc gcg acc gac ttc tca gag aaa acc 1059
Ile Val Thr Thr Ser Val Glu Thr Ala Thr Asp Phe Ser Glu Lys Thr
335 340 345

aag gtg gca aac acc acg acc gag ctc aac gac gga cgc gac gcc gga 1107
Lys Val Ala Asn Thr Thr Thr Glu Leu Asn Asp Gly Arg Asp Ala Gly
350 355 360 365

acg ggg atc ggt gcc gag cgc cac tgt gct gat gag aga tgg aaa gag 1155
Thr Gly Ile Gly Ala Glu Arg His Cys Ala Asp Glu Arg Trp Lys Glu
370 375 380

aca acg gta gcc ccc gat tgc gcc gta tcg gca gcg aac gcc tcg cga 1203
Thr Thr Val Ala Pro Asp Cys Ala Val Ser Ala Ala Asn Ala Ser Arg
385 390 395

cgc acc ggg gag ctg gcc acc ccg gtg acg atg ctg cct gat ccg ttg 1251
Arg Thr Gly Glu Leu Ala Thr Pro Val Thr Met Leu Pro Asp Pro Leu
400 405 410

tac gga ccg gaa taa aatcgcctga tgcct 1281
Tyr Gly Pro Glu
415

<210> 58
<211> 417
<212> PRT
<213> Arabidopsis thaliana

<400> 58
Met Ser Trp Arg Pro Arg Lys Asn Val Pro Met Lys Thr Arg Val Thr
1 5 10 15

Arg Asp Gly Ser Gly Pro Gly Lys Thr Gly Val Thr Arg Gly Ser Ser
20 25 30

Pro Met Arg Trp Ala Trp Lys Arg Trp Gln Ala Val Gly Ala Ser Thr
35 40 45

Ala Arg Thr Trp Phe Gly Thr Glu Asn Gln Lys Gly Ile Thr Thr Ser
50 55 60

Thr Arg Ala Arg Arg Tyr Ala Val Ser Ala Lys Phe Pro Arg Leu Ser
65 70 75 80

```
Asn Lys Gly Lys Asp Tyr Met Arg Cys Val Leu Gln Tyr Thr Val Lys
                85                  90                  95

Asn Glu Gln Lys Val Asp Cys Gly Gly Ser Tyr Ile Lys Leu Leu Pro
            100                 105                 110

Ser Lys Leu Arg Thr Gly Asp Gly Asp Gly Val Ser Glu Tyr Ser Ile
        115                 120                 125

Met Phe Gly Pro Asp Ser Thr Gly Ala Ser Arg Thr Val Arg Arg Ala
    130                 135                 140

Arg Asn Tyr Lys Gly Lys Arg His Leu Arg Lys Lys Glu Gln Asn Lys
145                 150                 155                 160

Val Glu Thr Asp Gln Leu Thr His Gln Tyr Thr Thr Ser Trp Ser Pro
                165                 170                 175

Asp Trp Thr Tyr Asn Val Leu Val Asp Asn Lys Glu Ser Gln Ala Gly
            180                 185                 190

Asn Leu Ala Asp Asp Cys Glu Leu Leu Pro Gln Lys Arg Ile Phe Arg
        195                 200                 205

Pro Ser Cys Arg Lys Gln Ser Lys Pro Val Thr Cys Val Asp Val Lys
    210                 215                 220

His His Ala Pro Arg Arg Asn Val Lys Pro Ala Gly His Asp Asp Ile
225                 230                 235                 240

Pro Ala Arg Arg Thr Thr Pro Glu Ala Val Arg Lys Gly Arg Thr Asn
                245                 250                 255

Glu Arg Pro Asp Arg Thr Trp Ala Thr Gly Thr Thr Pro Arg Pro Arg
            260                 265                 270

Arg Tyr Lys Gly Glu Thr Lys Ala Lys Lys His Pro Arg Pro Glu Tyr
        275                 280                 285

Lys Gly Thr Trp Val Thr Pro Leu Gln Asp Asn Pro Thr Pro Ala Pro
    290                 295                 300

Pro Asn Asp Leu Tyr Leu Phe Leu Asp Leu Gly Ala Ala Gly Thr Arg
305                 310                 315                 320

Thr Trp Thr Val Lys Ser Gly Ser Ile Thr Asn Asn Met Ile Val Thr
                325                 330                 335

Thr Ser Val Glu Thr Ala Thr Asp Phe Ser Glu Lys Thr Lys Val Ala
            340                 345                 350

Asn Thr Thr Thr Glu Leu Asn Asp Gly Arg Asp Ala Gly Thr Gly Ile
        355                 360                 365

Gly Ala Glu Arg His Cys Ala Asp Glu Arg Trp Lys Glu Thr Thr Val
    370                 375                 380
```

```
Ala Pro Asp Cys Ala Val Ser Ala Ala Asn Ala Ser Arg Arg Thr Gly
385                 390                 395                 400

Glu Leu Ala Thr Pro Val Thr Met Leu Pro Asp Pro Leu Tyr Gly Pro
                405                 410                 415

Glu


<210> 59
<211> 416
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)..(411)

<400> 59
aag gaa gct ttt agc ctc ttc gac aaa gat ggc gat ggt tgc atc aca      48
Lys Glu Ala Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Cys Ile Thr
  1               5                  10                  15

aca aaa gag ctg gga aca gtt atg cgt tca cta gga caa aac cca aca      96
Thr Lys Glu Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr
             20                  25                  30

gag gct gag ctc caa gac atg atc aac gag gtt gat gca gat gga aac     144
Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn
         35                  40                  45

ggc act atc gac ttc ccc gag ttc ctg aac ctg atg gct aag aag atg     192
Gly Thr Ile Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Lys Lys Met
     50                  55                  60

aaa gac act gac tcc gag gaa gag cta aaa gaa gcc ttc agg gtt ttc     240
Lys Asp Thr Asp Ser Glu Glu Glu Leu Lys Glu Ala Phe Arg Val Phe
 65                  70                  75                  80

gac aaa gac cag aac ggt ttc atc tcc gct gct gag cta cgc cat gtg     288
Asp Lys Asp Gln Asn Gly Phe Ile Ser Ala Ala Glu Leu Arg His Val
                 85                  90                  95

atg acc aat ctt ggt gag aag cta act gat gaa gaa gtg gaa gag atg     336
Met Thr Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Glu Glu Met
            100                 105                 110

atc cgt gag gct gat gtt gat gga gat ggt cag att aac tat gaa gag     384
Ile Arg Glu Ala Asp Val Asp Gly Asp Gly Gln Ile Asn Tyr Glu Glu
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35 40 45

Gly Thr Ile Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Lys Lys Met
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Lys Asp Thr Asp Ser Glu Glu Glu Leu Lys Glu Ala Phe Arg Val Phe
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Asp Lys Asp Gln Asn Gly Phe Ile Ser Ala Ala Glu Leu Arg His Val
85 90 95

Met Thr Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Glu Glu Met
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Asn Ser Ser Leu Ser Ser Gly Asn Gly Thr Glu Val Ala Thr Asp Val
        10                  15                  20

tct tct tgc ttc tat gtt ccc aat ccc tct gga acc gat ttc gat gcc   150
Ser Ser Cys Phe Tyr Val Pro Asn Pro Ser Gly Thr Asp Phe Asp Ala
    25                  30                  35

gag tcg tct tct ctt cct cct ct gtaagtcttc tttgaatttt taaaaacatt   203
Glu Ser Ser Ser Leu Pro Pro Le
 40                  45

cactctcttg ctgctgtctc tgttgatcct tcttctttga aaatttgaaa acattcttag 263

tctctcgctc tgtcacag c tcc cca gct cct caa gtg gca ttg tca att cct 315
                    u Ser Pro Ala Pro Gln Val Ala Leu Ser Ile Pro
                              50                  55

gcg gag ctt gcc gcc gcc att ccc ctc atc gat cgc ttc cag gtt gaa   363
Ala Glu Leu Ala Ala Ala Ile Pro Leu Ile Asp Arg Phe Gln Val Glu
    60                  65                  70

gct ttt ctg cgg cta atg cag aaa caa atc cag tct gct ggg aag cgt   411
Ala Phe Leu Arg Leu Met Gln Lys Gln Ile Gln Ser Ala Gly Lys Arg
 75                  80                  85                  90

ggc ttc ttc tat tcc aaa aag tcc tct ggc tcc aat gtc cgc gag cgc   459
Gly Phe Phe Tyr Ser Lys Lys Ser Ser Gly Ser Asn Val Arg Glu Arg
                 95                 100                 105

ttc aca ttt gag gat atg ctt tgc ttt caa aag gtttttcttt cccccccttt 512
Phe Thr Phe Glu Asp Met Leu Cys Phe Gln Lys
            110                 115

cttccccatt gacaatccat tgactg aat atg tct ctc tcc cct tcc ttc ctt   565
                             Asn Met Ser Leu Ser Pro Ser Phe Leu
                                     120                 125

cag gat cca atc ccc aca tct ctc ctc aag att aac agc gat ctc gtc   613
Gln Asp Pro Ile Pro Thr Ser Leu Leu Lys Ile Asn Ser Asp Leu Val
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Ser Arg Ala Thr Lys Leu Phe His Leu Ile Leu Lys Tyr Met Gly Val
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gat tca tct gat cga tct acg cct ccc agt tta gat gaa cgc att gac    709
Asp Ser Ser Asp Arg Ser Thr Pro Pro Ser Leu Asp Glu Arg Ile Asp
    160                 165                 170

ctc gtt gga aag ctc ttc aaa aaa act ttg aag cgt gtt gaa ctc agg    757
Leu Val Gly Lys Leu Phe Lys Lys Thr Leu Lys Arg Val Glu Leu Arg
175                 180                 185                     190

gac gaa ctt ttt gcc caa atc tcc aaa cag act aga cat aat cct gac    805
Asp Glu Leu Phe Ala Gln Ile Ser Lys Gln Thr Arg His Asn Pro Asp
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agg caa tac ttg atc aaa gct tgg gaa ttg atg tac tta tgt gcc tcc    853
Arg Gln Tyr Leu Ile Lys Ala Trp Glu Leu Met Tyr Leu Cys Ala Ser
            210                 215                 220

tct atg cct cct agc aaa gat atc ggt gga tat cta tct gag tat att    901
Ser Met Pro Pro Ser Lys Asp Ile Gly Gly Tyr Leu Ser Glu Tyr Ile
        225                 230                 235

cat aat gtc gca cac gat gca act att gaa ccg gat gct cag gtt ctt    949
His Asn Val Ala His Asp Ala Thr Ile Glu Pro Asp Ala Gln Val Leu
    240                 245                 250

gct gtt aac act ttg aaa gct tta aag cgc tct atc aaa gct ggt cct    997
Ala Val Asn Thr Leu Lys Ala Leu Lys Arg Ser Ile Lys Ala Gly Pro
255                 260                 265                 270

agg cac acc aca cct ggt cgt gaa gaa att gaa gcc ctt ttg acc ggt   1045
Arg His Thr Thr Pro Gly Arg Glu Glu Ile Glu Ala Leu Leu Thr Gly
                275                 280                 285

aga aag ctc aca acc att gtc ttc ttt ctc gat gaa act ttt gaa gaa   1093
Arg Lys Leu Thr Thr Ile Val Phe Phe Leu Asp Glu Thr Phe Glu Glu
            290                 295                 300

att tca tat gac atg gct acc aca gtg tct gat gct gtt gag           1135
Ile Ser Tyr Asp Met Ala Thr Thr Val Ser Asp Ala Val Glu
        305                 310                 315

gtatcttctt gctttctttt ttcataattt accgctgatc atattcttgt ccctttttct 1195

ctcactgcat tgacatctgt ttcaggag cta gct gga aca att aaa cta tca    1247
                               Leu Ala Gly Thr Ile Lys Leu Ser
                                               320

gct ttc tct agc ttt agt ttg ttt gaa tgt cgt aaa gtt gtt tca agt   1295
Ala Phe Ser Ser Phe Ser Leu Phe Glu Cys Arg Lys Val Val Ser Ser
325                 330                 335                 340

tct aaa tca tct gat ccc gga aat g gtatgctttc atatgactgg           1340
Ser Lys Ser Ser Asp Pro Gly Asn G
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cag ag gaa tat ata gga ttg gat gat aac aag tat att gga gat ctc    1447
    lu Glu Tyr Ile Gly Leu Asp Asp Asn Lys Tyr Ile Gly Asp Leu
       350                355                 360

ctc gca gaa ttt aaa gct att aaa gac cga aat aaa gga gag ata cta   1495
Leu Ala Glu Phe Lys Ala Ile Lys Asp Arg Asn Lys Gly Glu Ile Leu
    365                 370                 375

cac tgc aaa ctg gta ttt aaa aaa aaa tta ttc cga gag tct gat gaa   1543
His Cys Lys Leu Val Phe Lys Lys Lys Leu Phe Arg Glu Ser Asp Glu
380                 385                 390                 395

gct gta aca gat ctg atg ttt gtg caa ctt tcg tat gtt caa           1585
Ala Val Thr Asp Leu Met Phe Val Gln Leu Ser Tyr Val Gln
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gtgagcattt tcttcattgg tgacatttat ttccacacaa aaggcttgcc tttcgttgct 1645

gacacacata tatgcag ctg caa cat gac tat ttg cta gga aac tat cct   1695
                   Leu Gln His Asp Tyr Leu Leu Gly Asn Tyr Pro
                   410                 415                 420

gtt ggg agg gac gat gct gca cag ctt tgt gcc ttg caa att ctt gtt   1743
Val Gly Arg Asp Asp Ala Ala Gln Leu Cys Ala Leu Gln Ile Leu Val
                425                 430                 435

ggg att ggg ttt gtc aat agt cca gag tca tgc at gttagttttc         1788
Gly Ile Gly Phe Val Asn Ser Pro Glu Ser Cys Il
            440                 445

ttaagctccg ccattgactt tattttagtt gtccgatact ttatttttcc aattttcctc 1848

ccttaacaat atcatttcct ttctcaatgt atcacatatc ag t gat tgg aca tca  1903
                                               e Asp Trp Thr Ser
                                                     450

ctt ctt gag cgg ttt ttg cca aga caa ata gca ata acc cga gca aag   1951
Leu Leu Glu Arg Phe Leu Pro Arg Gln Ile Ala Ile Thr Arg Ala Lys
        455                 460                 465

cgt gaa tgg gaa ttg gat atc ctt gct cgc tac cgt tca atg           1993
Arg Glu Trp Glu Leu Asp Ile Leu Ala Arg Tyr Arg Ser Met
    470                 475                 480

gtaggaatag ttctatgcat gtggattgtc ttcccctttc tagatacctt tggcaaataa 2053

aaacccattg aagtgatggc atggtaaaat gatatttcgt atgtgtatgt gggcatgtag 2113

gag aac gtg acc aaa gat gat gca aga caa caa ttt cta cgg ata ctg   2161
Glu Asn Val Thr Lys Asp Asp Ala Arg Gln Gln Phe Leu Arg Ile Leu
        485                 490                 495

aag gca ctg cca tac ggg aat tca gtt ttt ttt agc gta cgc aag ata   2209
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Lys Ala Leu Pro Tyr Gly Asn Ser Val Phe Phe Ser Val Arg Lys Ile
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Asp Asp Pro Ile Gly Leu Leu Pro Gly Arg Ile Ile Leu Gly Ile Asn
515                 520                 525                 530

aaa cgt ggg gttgtctcaa tataaatgtt atacattatg actttaaaaa           2306
Lys Arg Gly

aactgttatt gttgtttgga attcaaatct atgttgttgg atttgaattt gttgtttgct 2366

ttcttgtag gtt cac ttt ttt cga ccg gtt cct aaa gaa tat ctg cac tct 2417
          Val His Phe Phe Arg Pro Val Pro Lys Glu Tyr Leu His Ser
              535                 540                 545

gct gaa cta cgt gac atc atg caa ttt ggc agc agt aac act gct gtc   2465
Ala Glu Leu Arg Asp Ile Met Gln Phe Gly Ser Ser Asn Thr Ala Val
        550                 555                 560

ttt ttc aaa atg aga gtc gct ggt gtt ctt cac ata ttt cag ttc gag   2513
Phe Phe Lys Met Arg Val Ala Gly Val Leu His Ile Phe Gln Phe Glu
    565                 570                 575

aca aaa cag gtttaaacat cactatttgt ggatcattat attatgaagc           2562
Thr Lys Gln
580

aattccttat gagatattca atttgggtaa cttgtatgtt tgtag gga gaa gaa att 2619
                                                  Gly Glu Glu Ile
                                                          585

tgt gtt gct ttg caa aca cat ata aat gat gtc atg ttg cgt cgt tac   2667
Cys Val Ala Leu Gln Thr His Ile Asn Asp Val Met Leu Arg Arg Tyr
            590                 595                 600

tcc aaa gct cga tct gct gcc aat tgc ttg gtt aat gga gat att tct   2715
Ser Lys Ala Arg Ser Ala Ala Asn Cys Leu Val Asn Gly Asp Ile Ser
        605                 610                 615

tgt tgt tct aag ccg caa aat ttt gaa gtg tat gaa aaa cgt ttg caa   2763
Cys Cys Ser Lys Pro Gln Asn Phe Glu Val Tyr Glu Lys Arg Leu Gln
    620                 625                 630

gat ttg tct aag gct tat gaa gag tcc caa aag aag att gag aag       2808
Asp Leu Ser Lys Ala Tyr Glu Glu Ser Gln Lys Lys Ile Glu Lys
635                 640                 645

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caa gaa gtt act ctg cgt gaa gag tta gaa gct ata cac aat ggt ttg     3148
Gln Glu Val Thr Leu Arg Glu Glu Leu Glu Ala Ile His Asn Gly Leu
660                 665                 670                 675

gag ctt gaa agg aga aaa ttg ttg gag gtt act tta gac cga gat aaa     3196
Glu Leu Glu Arg Arg Lys Leu Leu Glu Val Thr Leu Asp Arg Asp Lys
                680                 685                 690

ctt agg tca ttg tgt gac gag aag gga acc cct att caa gttagttata      3245
Leu Arg Ser Leu Cys Asp Glu Lys Gly Thr Pro Ile Gln
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acctaacttt tgtctttctt ttgatgcttg gttgaagtta tttaatgatt tattctatat 3305

atgctatag tcc ttg atg tct gaa ctg cga gga atg gaa gca agg ttg gca 3356
          Ser Leu Met Ser Glu Leu Arg Gly Met Glu Ala Arg Leu Ala
          705                 710                 715

aag tcg ggc aac acc aaa tca agt aaa gag acc aaa tca gaa tta gcc     3404
Lys Ser Gly Asn Thr Lys Ser Ser Lys Glu Thr Lys Ser Glu Leu Ala
    720                 725                 730

gaa atg aat aat cag gtgaatatta tgtgtttaaa tctaattcat tgtaatcatt     3459
Glu Met Asn Asn Gln
735

gagttgttgt tttttgttcc caattctgct ttcctttgac aatgaatttt aagtcacag    3518

ata tta tac aag atc caa aag gag tta gaa gtt cga aat aag gaa ttg     3566
Ile Leu Tyr Lys Ile Gln Lys Glu Leu Glu Val Arg Asn Lys Glu Leu
740                 745                 750                 755

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His Val Ala Val Asp Asn Ser Lys Arg Leu Leu Ser Glu Asn Lys Ile
                760                 765                 770

ttg gag caa aat ctc aat att gaa aag aag aaa aaa gag gag             3656
Leu Glu Gln Asn Leu Asn Ile Glu Lys Lys Lys Lys Glu Glu
            775                 780                 785

gtgaattcta tgtattagat ttattgaaga tttcaaattg agaagtatca aatacttgcg 3716

tattgttgac atctcattat ttcag gtt gaa att cat caa aag aga tat gaa     3768
                            Val Glu Ile His Gln Lys Arg Tyr Glu
                                            790

caa gaa aaa aag gtg tta aag ctt cga gtt tct gaa ctt gaa aat aag     3816
Gln Glu Lys Lys Val Leu Lys Leu Arg Val Ser Glu Leu Glu Asn Lys
795                 800                 805                 810

ctt gaa gta ctt gct caa gac ttg gat agt gct gag tct acg att gaa     3864
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            830                 835                 840

gag gag tta aga gaa atg aaa gag gtaatggtac tcttttgtct tcttcattat  3966
Glu Glu Leu Arg Glu Met Lys Glu
        845                 850

ttaattttgt ttctgtttga atgatgataa tgtattttcg cgattccaaa ttgaagtaga 4026

gggatgtgtt tacattccaa tttcattttc ttag gac att gac aga aaa aat gag 4081
                                      Asp Ile Asp Arg Lys Asn Glu
                                                      855

caa aca gct gcc att ttg aaa atg caa gga gcc caa ctt gct gag cta   4129
Gln Thr Ala Ala Ile Leu Lys Met Gln Gly Ala Gln Leu Ala Glu Leu
        860                 865                 870

gaa ata ctt tat aag gaa gaa caa gtt tta agg aaa aga tac tat aat   4177
Glu Ile Leu Tyr Lys Glu Glu Gln Val Leu Arg Lys Arg Tyr Tyr Asn
    875                 880                 885

acc ata gaa g gtaacataat gctcaagtat gtacaatgat gttcattgct         4227
Thr Ile Glu A
890

tttaaaaaag aattttacta acatttttat ttgattgtag at atg aaa ggg aag    4281
                                            sp Met Lys Gly Lys
                                                       895

att aga gtt tat tgt cga ata aga cct cta aat gaa aaa gag agt tca   4329
Ile Arg Val Tyr Cys Arg Ile Arg Pro Leu Asn Glu Lys Glu Ser Ser
        900                 905                 910

gag agg gaa aaa caa atg ctg aca act gtg gat gag ttt act gtt gaa   4377
Glu Arg Glu Lys Gln Met Leu Thr Thr Val Asp Glu Phe Thr Val Glu
    915                 920                 925

cat gca tgg aaa gac gac aaa aga aag caa cac ata tat gat cgc gta   4425
His Ala Trp Lys Asp Asp Lys Arg Lys Gln His Ile Tyr Asp Arg Val
930                 935                 940                 945

ttt gac atg cgt gct agt caa gat gat atc ttt gaa gac aca aag       4470
Phe Asp Met Arg Ala Ser Gln Asp Asp Ile Phe Glu Asp Thr Lys
                950                 955                 960

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actaacatcg ttttcctttt aacag tat ttg gta cag tcg gct gta gat ggg   4582
                            Tyr Leu Val Gln Ser Ala Val Asp Gly
                                            965

tat aac gtt tgc atc ttt gca tat ggt caa act ggt tct gga aaa act   4630
Tyr Asn Val Cys Ile Phe Ala Tyr Gly Gln Thr Gly Ser Gly Lys Thr
970                 975                 980                 985

ttc act ata tat ggg cat gag agc aat cct gga ctc aca cct cga gct   4678
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Phe Thr Ile Tyr Gly His Glu Ser Asn Pro Gly Leu Thr Pro Arg Ala
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Thr Lys Glu Leu Phe Asn Ile Leu Lys Arg Asp Ser Lys Arg Phe Ser
            1005                1010                1015

ttt tct cta aag gtaatttgtt atcctaatag atgatgtgat aaaagattat        4778
Phe Ser Leu Lys
        1020

gacatcaact gactacaaaa agttatgcag gca tat atg gtg gaa ctt tat caa   4832
                                 Ala Tyr Met Val Glu Leu Tyr Gln
                                             1025

gac aca ctt gta gac ctt ttg tta cca aaa agt gca aga cgc ttg aaa    4880
Asp Thr Leu Val Asp Leu Leu Leu Pro Lys Ser Ala Arg Arg Leu Lys
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cta gag att aaa aaa gat tca aag gtattgtgag atatatctat tttaactagg  4934
Leu Glu Ile Lys Lys Asp Ser Lys
                1050

ttataactag attgtagaca cgtaagtttg atcttatgca taaaatattt tctcag gga 4993
                                                              Gly

atg gtc ttt gta gag aat gtg aca act att cct ata tca act ttg gag    5041
Met Val Phe Val Glu Asn Val Thr Thr Ile Pro Ile Ser Thr Leu Glu
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gaa ctg cga atg att ctt gaa cgg gga tcg gaa cga cga cat gtt tct    5089
Glu Leu Arg Met Ile Leu Glu Arg Gly Ser Glu Arg Arg His Val Ser
                1075                1080                1085

gga aca aat atg aat gaa gaa agc tca aga tct cac ctc ata tta tca    5137
Gly Thr Asn Met Asn Glu Glu Ser Ser Arg Ser His Leu Ile Leu Ser
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gtt gtt att gaa agt att gat ctt caa acc cag tct gct gcg agg ggc    5185
Val Val Ile Glu Ser Ile Asp Leu Gln Thr Gln Ser Ala Ala Arg Gly
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aag gtgacaaaat tcactatgtt tttctttatt gactcattat cattttcac          5238
Lys

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atattctgaa tttttgtttg ttatttgcag ctg agt ttt gtg gat ctt gct ggt   5532
                                 Leu Ser Phe Val Asp Leu Ala Gly
                                1120                1125
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1130 1135 1140

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Ala Gln Ser Ile Asn Lys Ser Leu Ser Ala Leu Gly Asp Val Ile Gly
1145 1150 1155

gct tta tct tct ggc aac cag cat att cct tat agg aat cac aag cta 5676
Ala Leu Ser Ser Gly Asn Gln His Ile Pro Tyr Arg Asn His Lys Leu
1160 1165 1170 1175

acg atg ttg atg agc gat tca ttg ggc ggc aat gcc aag acg tta atg 5724
Thr Met Leu Met Ser Asp Ser Leu Gly Gly Asn Ala Lys Thr Leu Met
1180 1185 1190

ttt gtt aat gtg tct cca gcc gaa tca aat ttg gac gag acg tac aat 5772
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1195 1200 1205

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u Tyr Ala
1210

tcg aga gtg aga acg atc gtg aat gat ccc agc aaa cat ata tca tcc 5933
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1215 1220 1225

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gcc ggt aaa aaa ggt gag gaa gaa gac ttg gtg gat att gag gaa gat 6029
Ala Gly Lys Lys Gly Glu Glu Glu Asp Leu Val Asp Ile Glu Glu Asp
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Pro Ala Pro Gln Val Ala Leu Ser Ile Pro Ala Glu Leu Ala Ala Ala
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Ile Pro Leu Ile Asp Arg Phe Gln Val Glu Ala Phe Leu Arg Leu Met
65                      70                      75                      80

Gln Lys Gln Ile Gln Ser Ala Gly Lys Arg Gly Phe Phe Tyr Ser Lys
                85                      90                      95

Lys Ser Ser Gly Ser Asn Val Arg Glu Arg Phe Thr Phe Glu Asp Met
            100                     105                     110

Leu Cys Phe Gln Lys Asn Met Ser Leu Ser Pro Ser Phe Leu Gln Asp
        115                     120                     125

Pro Ile Pro Thr Ser Leu Leu Lys Ile Asn Ser Asp Leu Val Ser Arg
    130                     135                     140

Ala Thr Lys Leu Phe His Leu Ile Leu Lys Tyr Met Gly Val Asp Ser
145                     150                     155                     160

Ser Asp Arg Ser Thr Pro Pro Ser Leu Asp Glu Arg Ile Asp Leu Val
                165                     170                     175

Gly Lys Leu Phe Lys Lys Thr Leu Lys Arg Val Glu Leu Arg Asp Glu
            180                     185                     190

Leu Phe Ala Gln Ile Ser Lys Gln Thr Arg His Asn Pro Asp Arg Gln
        195                     200                     205

Tyr Leu Ile Lys Ala Trp Glu Leu Met Tyr Leu Cys Ala Ser Ser Met
    210                     215                     220

Pro Pro Ser Lys Asp Ile Gly Gly Tyr Leu Ser Glu Tyr Ile His Asn
225                     230                     235                     240

Val Ala His Asp Ala Thr Ile Glu Pro Asp Ala Gln Val Leu Ala Val
                245                     250                     255

Asn Thr Leu Lys Ala Leu Lys Arg Ser Ile Lys Ala Gly Pro Arg His
            260                     265                     270

Thr Thr Pro Gly Arg Glu Glu Ile Glu Ala Leu Leu Thr Gly Arg Lys
        275                     280                     285

Leu Thr Thr Ile Val Phe Phe Leu Asp Glu Thr Phe Glu Glu Ile Ser
    290                     295                     300

Tyr Asp Met Ala Thr Thr Val Ser Asp Ala Val Glu Leu Ala Gly Thr
305                     310                     315                     320

Ile Lys Leu Ser Ala Phe Ser Ser Phe Ser Leu Phe Glu Cys Arg Lys
                325                     330                     335

Val Val Ser Ser Ser Lys Ser Ser Asp Pro Gly Asn Glu Glu Tyr Ile
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340 345 350

Gly Leu Asp Asp Asn Lys Tyr Ile Gly Asp Leu Leu Ala Glu Phe Lys
355 360 365

Ala Ile Lys Asp Arg Asn Lys Gly Glu Ile Leu His Cys Lys Leu Val
370 375 380

Phe Lys Lys Lys Leu Phe Arg Glu Ser Asp Glu Ala Val Thr Asp Leu
385 390 395 400

Met Phe Val Gln Leu Ser Tyr Val Gln Leu Gln His Asp Tyr Leu Leu
405 410 415

Gly Asn Tyr Pro Val Gly Arg Asp Asp Ala Ala Gln Leu Cys Ala Leu
420 425 430

Gln Ile Leu Val Gly Ile Gly Phe Val Asn Ser Pro Glu Ser Cys Ile
435 440 445

Asp Trp Thr Ser Leu Leu Glu Arg Phe Leu Pro Arg Gln Ile Ala Ile
450 455 460

Thr Arg Ala Lys Arg Glu Trp Glu Leu Asp Ile Leu Ala Arg Tyr Arg
465 470 475 480

Ser Met Glu Asn Val Thr Lys Asp Asp Ala Arg Gln Gln Phe Leu Arg
485 490 495

Ile Leu Lys Ala Leu Pro Tyr Gly Asn Ser Val Phe Phe Ser Val Arg
500 505 510

Lys Ile Asp Asp Pro Ile Gly Leu Leu Pro Gly Arg Ile Ile Leu Gly
515 520 525

Ile Asn Lys Arg Gly Val His Phe Phe Arg Pro Val Pro Lys Glu Tyr
530 535 540

Leu His Ser Ala Glu Leu Arg Asp Ile Met Gln Phe Gly Ser Ser Asn
545 550 555 560

Thr Ala Val Phe Phe Lys Met Arg Val Ala Gly Val Leu His Ile Phe
565 570 575

Gln Phe Glu Thr Lys Gln Gly Glu Glu Ile Cys Val Ala Leu Gln Thr
580 585 590

His Ile Asn Asp Val Met Leu Arg Arg Tyr Ser Lys Ala Arg Ser Ala
595 600 605

Ala Asn Cys Leu Val Asn Gly Asp Ile Ser Cys Cys Ser Lys Pro Gln
610 615 620

Asn Phe Glu Val Tyr Glu Lys Arg Leu Gln Asp Leu Ser Lys Ala Tyr
625 630 635 640

Glu Glu Ser Gln Lys Lys Ile Glu Lys Leu Met Asp Glu Gln Gln Glu

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                645                 650                 655
Lys Asn Gln Gln Glu Val Thr Leu Arg Glu Glu Leu Glu Ala Ile His
            660                 665                 670

Asn Gly Leu Glu Leu Glu Arg Arg Lys Leu Leu Glu Val Thr Leu Asp
        675                 680                 685

Arg Asp Lys Leu Arg Ser Leu Cys Asp Glu Lys Gly Thr Pro Ile Gln
    690                 695                 700

Ser Leu Met Ser Glu Leu Arg Gly Met Glu Ala Arg Leu Ala Lys Ser
705                 710                 715                 720

Gly Asn Thr Lys Ser Ser Lys Glu Thr Lys Ser Glu Leu Ala Glu Met
                725                 730                 735

Asn Asn Gln Ile Leu Tyr Lys Ile Gln Lys Glu Leu Glu Val Arg Asn
            740                 745                 750

Lys Glu Leu His Val Ala Val Asp Asn Ser Lys Arg Leu Leu Ser Glu
        755                 760                 765

Asn Lys Ile Leu Glu Gln Asn Leu Asn Ile Glu Lys Lys Lys Lys Glu
    770                 775                 780

Glu Val Glu Ile His Gln Lys Arg Tyr Glu Gln Glu Lys Lys Val Leu
785                 790                 795                 800

Lys Leu Arg Val Ser Glu Leu Glu Asn Lys Leu Glu Val Leu Ala Gln
                805                 810                 815

Asp Leu Asp Ser Ala Glu Ser Thr Ile Glu Ser Lys Asn Ser Asp Met
            820                 825                 830

Leu Leu Leu Gln Asn Asn Leu Lys Glu Leu Glu Glu Leu Arg Glu Met
        835                 840                 845

Lys Glu Asp Ile Asp Arg Lys Asn Glu Gln Thr Ala Ala Ile Leu Lys
    850                 855                 860

Met Gln Gly Ala Gln Leu Ala Glu Leu Glu Ile Leu Tyr Lys Glu Glu
865                 870                 875                 880

Gln Val Leu Arg Lys Arg Tyr Tyr Asn Thr Ile Glu Asp Met Lys Gly
                885                 890                 895

Lys Ile Arg Val Tyr Cys Arg Ile Arg Pro Leu Asn Glu Lys Glu Ser
            900                 905                 910

Ser Glu Arg Glu Lys Gln Met Leu Thr Thr Val Asp Glu Phe Thr Val
        915                 920                 925

Glu His Ala Trp Lys Asp Asp Lys Arg Lys Gln His Ile Tyr Asp Arg
    930                 935                 940

Val Phe Asp Met Arg Ala Ser Gln Asp Asp Ile Phe Glu Asp Thr Lys
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945 950 955 960

Tyr Leu Val Gln Ser Ala Val Asp Gly Tyr Asn Val Cys Ile Phe Ala
965 970 975

Tyr Gly Gln Thr Gly Ser Gly Lys Thr Phe Thr Ile Tyr Gly His Glu
980 985 990

Ser Asn Pro Gly Leu Thr Pro Arg Ala Thr Lys Glu Leu Phe Asn Ile
995 1000 1005

Leu Lys Arg Asp Ser Lys Arg Phe Ser Phe Ser Leu Lys Ala Tyr Met
1010 1015 1020

Val Glu Leu Tyr Gln Asp Thr Leu Val Asp Leu Leu Leu Pro Lys Ser
025 1030 1035 1040

Ala Arg Arg Leu Lys Leu Glu Ile Lys Lys Asp Ser Lys Gly Met Val
1045 1050 1055

Phe Val Glu Asn Val Thr Thr Ile Pro Ile Ser Thr Leu Glu Glu Leu
1060 1065 1070

Arg Met Ile Leu Glu Arg Gly Ser Glu Arg Arg His Val Ser Gly Thr
1075 1080 1085

Asn Met Asn Glu Glu Ser Ser Arg Ser His Leu Ile Leu Ser Val Val
1090 1095 1100

Ile Glu Ser Ile Asp Leu Gln Thr Gln Ser Ala Ala Arg Gly Lys Leu
105 1110 1115 1120

Ser Phe Val Asp Leu Ala Gly Ser Glu Arg Val Lys Lys Ser Gly Ser
1125 1130 1135

Ala Gly Cys Gln Leu Lys Glu Ala Gln Ser Ile Asn Lys Ser Leu Ser
1140 1145 1150

Ala Leu Gly Asp Val Ile Gly Ala Leu Ser Ser Gly Asn Gln His Ile
1155 1160 1165

Pro Tyr Arg Asn His Lys Leu Thr Met Leu Met Ser Asp Ser Leu Gly
1170 1175 1180

Gly Asn Ala Lys Thr Leu Met Phe Val Asn Val Ser Pro Ala Glu Ser
185 1190 1195 1200

Asn Leu Asp Glu Thr Tyr Asn Ser Leu Leu Tyr Ala Ser Arg Val Arg
1205 1210 1215

Thr Ile Val Asn Asp Pro Ser Lys His Ile Ser Ser Lys Glu Met Val
1220 1225 1230

Arg Leu Lys Lys Leu Val Ala Tyr Trp Lys Glu Gln Ala Gly Lys Lys
1235 1240 1245

Gly Glu Glu Glu Asp Leu Val Asp Ile Glu Glu Asp Arg Thr Arg Lys

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Asp Glu Ala Asp Ser
265


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<400> 63
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Met Asn Thr Asp Lys Met Thr Lys Met Asp Leu Thr Gly Ser Asn Asn
  1               5                  10                  15

gtg ccc att aat cca ccg acc act aag cgt gat ctt aga cag aat gat    96
Val Pro Ile Asn Pro Pro Thr Thr Lys Arg Asp Leu Arg Gln Asn Asp
             20                  25                  30

aat aat aac cct aag agt cat aat agt cat aat agc aat ggg atg act   144
Asn Asn Asn Pro Lys Ser His Asn Ser His Asn Ser Asn Gly Met Thr
         35                  40                  45

ggt aac agg aac aat aat aat aaa aat gcc ggc gga gtt gaa act agt   192
Gly Asn Arg Asn Asn Asn Asn Lys Asn Ala Gly Gly Val Glu Thr Ser
     50                  55                  60

aaa aaa gcg cgc tca cga ctg gaa aca cat ccc cga gat aat gag aat   240
Lys Lys Ala Arg Ser Arg Leu Glu Thr His Pro Arg Asp Asn Glu Asn
 65                  70                  75                  80

aat tac aga cta gct aca agt gcc ggt acg aaa gga ggt gcg cga acc   288
Asn Tyr Arg Leu Ala Thr Ser Ala Gly Thr Lys Gly Gly Ala Arg Thr
                 85                  90                  95

gtt gac gta cca gtc ata tta agt acc cgg gaa tca caa ggc aca cgt   336
Val Asp Val Pro Val Ile Leu Ser Thr Arg Glu Ser Gln Gly Thr Arg
            100                 105                 110

tca gta aat gca aca agt aaa att aga tgc ccg gat tcc act gca att   384
Ser Val Asn Ala Thr Ser Lys Ile Arg Cys Pro Asp Ser Thr Ala Ile
        115                 120                 125

tgc gag tgg ttc gcc acg ccc acg gat cct caa aga cca gga gtt tat   432
Cys Glu Trp Phe Ala Thr Pro Thr Asp Pro Gln Arg Pro Gly Val Tyr
    130                 135                 140

aac cac aag aac ggc gac aaa aac aac aga gat acc ggg aac att aat   480
Asn His Lys Asn Gly Asp Lys Asn Asn Arg Asp Thr Gly Asn Ile Asn
145                 150                 155                 160
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acc gtt agc agt cta atg gat aat gct agg ggt ccg aac ccg cga tct 528
Thr Val Ser Ser Leu Met Asp Asn Ala Arg Gly Pro Asn Pro Arg Ser
165 170 175

ggg att tca ata ccg aca cca acc tct aga caa tcc cca agt gag aca 576
Gly Ile Ser Ile Pro Thr Pro Thr Ser Arg Gln Ser Pro Ser Glu Thr
180 185 190

cct cca gat cca ctg cag aat cct aat aat tat act agg tat cat aat 624
Pro Pro Asp Pro Leu Gln Asn Pro Asn Asn Tyr Thr Arg Tyr His Asn
195 200 205

gat aaa aac agc aag aat agt aac aga aac tac aat aag aga aat aag 672
Asp Lys Asn Ser Lys Asn Ser Asn Arg Asn Tyr Asn Lys Arg Asn Lys
210 215 220

aac tcg acg acc ttt aat aac tcg gac ctt cct ggt cat aat aga agc 720
Asn Ser Thr Thr Phe Asn Asn Ser Asp Leu Pro Gly His Asn Arg Ser
225 230 235 240

tcc cct gcg att aat gca gta aaa tca gca tca aat cga tca tct gct 768
Ser Pro Ala Ile Asn Ala Val Lys Ser Ala Ser Asn Arg Ser Ser Ala
245 250 255

ata ggt agt cga aac agt gat tta aac aat gct gct aat gat gaa cgc 816
Ile Gly Ser Arg Asn Ser Asp Leu Asn Asn Ala Ala Asn Asp Glu Arg
260 265 270

cat tac gct aga tcg gga aca tat cag ata aac gct gta aca gta ctt 864
His Tyr Ala Arg Ser Gly Thr Tyr Gln Ile Asn Ala Val Thr Val Leu
275 280 285

aga gta tta gga aga gga gca cgg cgt gat gta aag tca gca tat cat 912
Arg Val Leu Gly Arg Gly Ala Arg Arg Asp Val Lys Ser Ala Tyr His
290 295 300

ggc acc tgt ggt aca ggt ccc cgg atg aaa gtg ata aca ttg gct gtt 960
Gly Thr Cys Gly Thr Gly Pro Arg Met Lys Val Ile Thr Leu Ala Val
305 310 315 320

caa gag aat att aga aac cga att ata ttg gag cta cgg aca tta cac 1008
Gln Glu Asn Ile Arg Asn Arg Ile Ile Leu Glu Leu Arg Thr Leu His
325 330 335

aag acc tct tat caa tat atc gtt ccg tat tat gat ggg atc tat aca 1056
Lys Thr Ser Tyr Gln Tyr Ile Val Pro Tyr Tyr Asp Gly Ile Tyr Thr
340 345 350

gag ggc tca att ttc att cgg atg gtg gaa ctt gga tgg gta acg aat 1104
Glu Gly Ser Ile Phe Ile Arg Met Val Glu Leu Gly Trp Val Thr Asn
355 360 365

atc atg aac aaa acg gcg acc ata cgt gcg ccg gtt ttg ggt acg atg 1152
Ile Met Asn Lys Thr Ala Thr Ile Arg Ala Pro Val Leu Gly Thr Met
370 375 380

gca ttt cta gtg tta caa ggt cgg att tac gtt cac aga aag ttc gat 1200

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Ala Phe Leu Val Leu Gln Gly Arg Ile Tyr Val His Arg Lys Phe Asp
385                 390                 395                 400

aaa tgc ccg agc aag cgt gat ata aaa cct tca gat att ctg gta aac     1248
Lys Cys Pro Ser Lys Arg Asp Ile Lys Pro Ser Asp Ile Leu Val Asn
                405                 410                 415

aat gaa ggt cga gca aag atc gca ggt ttc ggt gta agc gga cag tta     1296
Asn Glu Gly Arg Ala Lys Ile Ala Gly Phe Gly Val Ser Gly Gln Leu
            420                 425                 430

caa cat act ctc tca aag gat gta act tcg gtg gag tct cct gaa cgt     1344
Gln His Thr Leu Ser Lys Asp Val Thr Ser Val Glu Ser Pro Glu Arg
        435                 440                 445

cgt agt ggt agg tct tat ggt ttc gat cga gat att tgg agt gat ggt     1392
Arg Ser Gly Arg Ser Tyr Gly Phe Asp Arg Asp Ile Trp Ser Asp Gly
    450                 455                 460

ata aca cgt gta tca tgc gca atc ggg aga ttc cct tat gct tgt aat     1440
Ile Thr Arg Val Ser Cys Ala Ile Gly Arg Phe Pro Tyr Ala Cys Asn
465                 470                 475                 480

tac cca caa cag ctc cca caa gca tca caa cac cag cta cag caa cag     1488
Tyr Pro Gln Gln Leu Pro Gln Ala Ser Gln His Gln Leu Gln Gln Gln
                485                 490                 495

caa caa aaa cga ccg gcg tta caa cca aag caa gaa caa ccg gaa gta     1536
Gln Gln Lys Arg Pro Ala Leu Gln Pro Lys Gln Glu Gln Pro Glu Val
            500                 505                 510

gag aaa cac cga tta caa ata cca cgt caa aat tta gct gta tat aat     1584
Glu Lys His Arg Leu Gln Ile Pro Arg Gln Asn Leu Ala Val Tyr Asn
        515                 520                 525

agt aat cac gat ata tgg aat aat cgc aat aga gat aaa tat att att     1632
Ser Asn His Asp Ile Trp Asn Asn Arg Asn Arg Asp Lys Tyr Ile Ile
    530                 535                 540

agt aac aat cct aat aat agg aat gat aat aat aac act gta tgc gat     1680
Ser Asn Asn Pro Asn Asn Arg Asn Asp Asn Asn Asn Thr Val Cys Asp
545                 550                 555                 560

cta agc agt ggc gag tta ggt gaa agt cgt gag gtt gtg cca gac ggt     1728
Leu Ser Ser Gly Glu Leu Gly Glu Ser Arg Glu Val Val Pro Asp Gly
                565                 570                 575

atc ggg ttg gag gta ctt cta gat tct atc gta aaa gaa gag gta cga     1776
Ile Gly Leu Glu Val Leu Leu Asp Ser Ile Val Lys Glu Glu Val Arg
            580                 585                 590

atg gaa cca tca aca gtt tcg aag gaa ttt agg tcg atc att tct gaa     1824
Met Glu Pro Ser Thr Val Ser Lys Glu Phe Arg Ser Ile Ile Ser Glu
        595                 600                 605

tgt tta cga aac gat gca act gaa aga caa aca gct tca aac tta gta     1872
Cys Leu Arg Asn Asp Ala Thr Glu Arg Gln Thr Ala Ser Asn Leu Val
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    610                 615                 620

aat cac gaa ttt gta aag aaa tat caa aag tac aat cgt gaa aaa tgg   1920
Asn His Glu Phe Val Lys Lys Tyr Gln Lys Tyr Asn Arg Glu Lys Trp
625                 630                 635                 640

acc gca gat tta caa agg tgg caa taa aaatcgcctt cacgcctgat         1967
Thr Ala Asp Leu Gln Arg Trp Gln
                645

cgctgacgct cgacgcctgc ccccagcctg cagctcgccc agctcgccca ggctcgccca 2027

gcctgcccac cagcctgccc caccgctcca cgcctaaata ataaaaattt ttaaaaaaaa 2087

aaaaaaaaaa aaaccgct                                               2105


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Val Pro Ile Asn Pro Pro Thr Thr Lys Arg Asp Leu Arg Gln Asn Asp
             20                  25                  30

Asn Asn Asn Pro Lys Ser His Asn Ser His Asn Ser Asn Gly Met Thr
         35                  40                  45

Gly Asn Arg Asn Asn Asn Asn Lys Asn Ala Gly Gly Val Glu Thr Ser
     50                  55                  60

Lys Lys Ala Arg Ser Arg Leu Glu Thr His Pro Arg Asp Asn Glu Asn
 65                  70                  75                  80

Asn Tyr Arg Leu Ala Thr Ser Ala Gly Thr Lys Gly Gly Ala Arg Thr
                 85                  90                  95

Val Asp Val Pro Val Ile Leu Ser Thr Arg Glu Ser Gln Gly Thr Arg
            100                 105                 110

Ser Val Asn Ala Thr Ser Lys Ile Arg Cys Pro Asp Ser Thr Ala Ile
        115                 120                 125

Cys Glu Trp Phe Ala Thr Pro Thr Asp Pro Gln Arg Pro Gly Val Tyr
    130                 135                 140

Asn His Lys Asn Gly Asp Lys Asn Asn Arg Asp Thr Gly Asn Ile Asn
145                 150                 155                 160

Thr Val Ser Ser Leu Met Asp Asn Ala Arg Gly Pro Asn Pro Arg Ser
                165                 170                 175

Gly Ile Ser Ile Pro Thr Pro Thr Ser Arg Gln Ser Pro Ser Glu Thr
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180 185 190

Pro Pro Asp Pro Leu Gln Asn Pro Asn Asn Tyr Thr Arg Tyr His Asn
195 200 205

Asp Lys Asn Ser Lys Asn Ser Asn Arg Asn Tyr Asn Lys Arg Asn Lys
210 215 220

Asn Ser Thr Thr Phe Asn Asn Ser Asp Leu Pro Gly His Asn Arg Ser
225 230 235 240

Ser Pro Ala Ile Asn Ala Val Lys Ser Ala Ser Asn Arg Ser Ser Ala
245 250 255

Ile Gly Ser Arg Asn Ser Asp Leu Asn Asn Ala Ala Asn Asp Glu Arg
260 265 270

His Tyr Ala Arg Ser Gly Thr Tyr Gln Ile Asn Ala Val Thr Val Leu
275 280 285

Arg Val Leu Gly Arg Gly Ala Arg Arg Asp Val Lys Ser Ala Tyr His
290 295 300

Gly Thr Cys Gly Thr Gly Pro Arg Met Lys Val Ile Thr Leu Ala Val
305 310 315 320

Gln Glu Asn Ile Arg Asn Arg Ile Ile Leu Glu Leu Arg Thr Leu His
325 330 335

Lys Thr Ser Tyr Gln Tyr Ile Val Pro Tyr Tyr Asp Gly Ile Tyr Thr
340 345 350

Glu Gly Ser Ile Phe Ile Arg Met Val Glu Leu Gly Trp Val Thr Asn
355 360 365

Ile Met Asn Lys Thr Ala Thr Ile Arg Ala Pro Val Leu Gly Thr Met
370 375 380

Ala Phe Leu Val Leu Gln Gly Arg Ile Tyr Val His Arg Lys Phe Asp
385 390 395 400

Lys Cys Pro Ser Lys Arg Asp Ile Lys Pro Ser Asp Ile Leu Val Asn
405 410 415

Asn Glu Gly Arg Ala Lys Ile Ala Gly Phe Gly Val Ser Gly Gln Leu
420 425 430

Gln His Thr Leu Ser Lys Asp Val Thr Ser Val Glu Ser Pro Glu Arg
435 440 445

Arg Ser Gly Arg Ser Tyr Gly Phe Asp Arg Asp Ile Trp Ser Asp Gly
450 455 460

Ile Thr Arg Val Ser Cys Ala Ile Gly Arg Phe Pro Tyr Ala Cys Asn
465 470 475 480

Tyr Pro Gln Gln Leu Pro Gln Ala Ser Gln His Gln Leu Gln Gln Gln

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                485                 490                 495

Gln Gln Lys Arg Pro Ala Leu Gln Pro Lys Gln Glu Gln Pro Glu Val
            500                 505                 510

Glu Lys His Arg Leu Gln Ile Pro Arg Gln Asn Leu Ala Val Tyr Asn
        515                 520                 525

Ser Asn His Asp Ile Trp Asn Asn Arg Asn Arg Asp Lys Tyr Ile Ile
    530                 535                 540

Ser Asn Asn Pro Asn Asn Arg Asn Asp Asn Asn Asn Thr Val Cys Asp
545                 550                 555                 560

Leu Ser Ser Gly Glu Leu Gly Glu Ser Arg Glu Val Val Pro Asp Gly
                565                 570                 575

Ile Gly Leu Glu Val Leu Leu Asp Ser Ile Val Lys Glu Glu Val Arg
            580                 585                 590

Met Glu Pro Ser Thr Val Ser Lys Glu Phe Arg Ser Ile Ile Ser Glu
        595                 600                 605

Cys Leu Arg Asn Asp Ala Thr Glu Arg Gln Thr Ala Ser Asn Leu Val
    610                 615                 620

Asn His Glu Phe Val Lys Lys Tyr Gln Lys Tyr Asn Arg Glu Lys Trp
625                 630                 635                 640

Thr Ala Asp Leu Gln Arg Trp Gln
                645


<210> 65
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<212> DNA
<213> Arabidopsis thaliana

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                            Met Glu Gly Leu Ala Ile Arg Ala Ser
                             1               5

cga ccg tcg gtt ttc tgt tct att cca ggt ctc ggc ggc gat tcc cac   100
Arg Pro Ser Val Phe Cys Ser Ile Pro Gly Leu Gly Gly Asp Ser His
 10                  15                  20                  25

cga aaa cct cca agt gac ggt ttc ctc aag ctg cct gcg tcg tct att   148
Arg Lys Pro Pro Ser Asp Gly Phe Leu Lys Leu Pro Ala Ser Ser Ile
                 30                  35                  40

ccg gcg gac agc cga aaa tta gta gcg aat tct act tcc ttt cat cca   196
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Pro Ala Asp Ser Arg Lys Leu Val Ala Asn Ser Thr Ser Phe His Pro
            45                  50                  55

atc tca gcc gtt aac gtc tct gct caa gct tcc ctc acc gct gat ttt     244
Ile Ser Ala Val Asn Val Ser Ala Gln Ala Ser Leu Thr Ala Asp Phe
        60                  65                  70

ccc gcc ctt tca gaa act ata ctg aaa gag gga aga aat aac gga aaa     292
Pro Ala Leu Ser Glu Thr Ile Leu Lys Glu Gly Arg Asn Asn Gly Lys
    75                  80                  85

gag aaa gca gag aac atc gtg tgg cac gag agt tcg ata tgc aga tgc     340
Glu Lys Ala Glu Asn Ile Val Trp His Glu Ser Ser Ile Cys Arg Cys
90                  95                  100                 105

gac aga caa caa ctt ctt caa caa aag ggt tgt gtc gtt tgg atc act     388
Asp Arg Gln Gln Leu Leu Gln Gln Lys Gly Cys Val Val Trp Ile Thr
                110                 115                 120

ggt ctc agt ggt tca ggg aaa agc act gtt gct tgt gca cta agt aaa     436
Gly Leu Ser Gly Ser Gly Lys Ser Thr Val Ala Cys Ala Leu Ser Lys
            125                 130                 135

gca ttg ttt gaa aga ggc aaa ctt act tac aca ctc gac ggc gac aat     484
Ala Leu Phe Glu Arg Gly Lys Leu Thr Tyr Thr Leu Asp Gly Asp Asn
        140                 145                 150

gtc cgt cac ggc ctt aac cgt gac ctc act ttc aaa gca gag cac cgc     532
Val Arg His Gly Leu Asn Arg Asp Leu Thr Phe Lys Ala Glu His Arg
    155                 160                 165

acc gaa aac att aga aga att ggt gag gtg gct aag ttg ttt gct gac     580
Thr Glu Asn Ile Arg Arg Ile Gly Glu Val Ala Lys Leu Phe Ala Asp
170                 175                 180                 185

gtc gga gtc att tgt ata gca agt ttg att tct ccg tac cgg aga gac     628
Val Gly Val Ile Cys Ile Ala Ser Leu Ile Ser Pro Tyr Arg Arg Asp
                190                 195                 200

aga gac gcg tgc cgg tcc ttg tta cct gac ggc gat ttc gtc gag gtc     676
Arg Asp Ala Cys Arg Ser Leu Leu Pro Asp Gly Asp Phe Val Glu Val
            205                 210                 215

ttc atg gac gtt cct ctt cat gtg tgc gag tcg aga gat cca aag ggg     724
Phe Met Asp Val Pro Leu His Val Cys Glu Ser Arg Asp Pro Lys Gly
        220                 225                 230

ttg tac aag ctt gca cgt gca ggc aaa atc aaa ggc ttc act gga atc     772
Leu Tyr Lys Leu Ala Arg Ala Gly Lys Ile Lys Gly Phe Thr Gly Ile
    235                 240                 245

gac gac cct tac gag gca cca gtg aat tgc gag gta gtg ctg aaa cac     820
Asp Asp Pro Tyr Glu Ala Pro Val Asn Cys Glu Val Val Leu Lys His
250                 255                 260                 265

aca gga gac gac gag tcg tgt tcg cca cgt cag atg gct gag aac atc     868
Thr Gly Asp Asp Glu Ser Cys Ser Pro Arg Gln Met Ala Glu Asn Ile
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                270                 275                 280

atc tct tac ctg caa aac aaa ggt tat ctt gag ggc taa gtcaaagtcg     917
Ile Ser Tyr Leu Gln Asn Lys Gly Tyr Leu Glu Gly
            285                 290

gaa                                                                920


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<211> 293
<212> PRT
<213> Arabidopsis thaliana

<400> 66
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  1               5                  10                  15

Ile Pro Gly Leu Gly Gly Asp Ser His Arg Lys Pro Pro Ser Asp Gly
             20                  25                  30

Phe Leu Lys Leu Pro Ala Ser Ser Ile Pro Ala Asp Ser Arg Lys Leu
         35                  40                  45

Val Ala Asn Ser Thr Ser Phe His Pro Ile Ser Ala Val Asn Val Ser
     50                  55                  60

Ala Gln Ala Ser Leu Thr Ala Asp Phe Pro Ala Leu Ser Glu Thr Ile
 65                  70                  75                  80

Leu Lys Glu Gly Arg Asn Asn Gly Lys Glu Lys Ala Glu Asn Ile Val
                 85                  90                  95

Trp His Glu Ser Ser Ile Cys Arg Cys Asp Arg Gln Gln Leu Leu Gln
            100                 105                 110

Gln Lys Gly Cys Val Val Trp Ile Thr Gly Leu Ser Gly Ser Gly Lys
        115                 120                 125

Ser Thr Val Ala Cys Ala Leu Ser Lys Ala Leu Phe Glu Arg Gly Lys
    130                 135                 140

Leu Thr Tyr Thr Leu Asp Gly Asp Asn Val Arg His Gly Leu Asn Arg
145                 150                 155                 160

Asp Leu Thr Phe Lys Ala Glu His Arg Thr Glu Asn Ile Arg Arg Ile
                165                 170                 175

Gly Glu Val Ala Lys Leu Phe Ala Asp Val Gly Val Ile Cys Ile Ala
            180                 185                 190

Ser Leu Ile Ser Pro Tyr Arg Arg Asp Arg Asp Ala Cys Arg Ser Leu
        195                 200                 205

Leu Pro Asp Gly Asp Phe Val Glu Val Phe Met Asp Val Pro Leu His
    210                 215                 220
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Val Cys Glu Ser Arg Asp Pro Lys Gly Leu Tyr Lys Leu Ala Arg Ala
225                 230                 235                 240

Gly Lys Ile Lys Gly Phe Thr Gly Ile Asp Asp Pro Tyr Glu Ala Pro
                245                 250                 255

Val Asn Cys Glu Val Val Leu Lys His Thr Gly Asp Asp Glu Ser Cys
            260                 265                 270

Ser Pro Arg Gln Met Ala Glu Asn Ile Ile Ser Tyr Leu Gln Asn Lys
        275                 280                 285

Gly Tyr Leu Glu Gly
    290
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<211> 1257
<212> DNA
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<222> (13)..(1245)

<400> 67

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              Met Gly Ile Cys Leu Ser Ala Gln Val Lys Ala Glu Ser
                1               5                  10

tca gga gcg agt acg aag tat gac gcc aaa gat ata gga agt ctt ggg   99
Ser Gly Ala Ser Thr Lys Tyr Asp Ala Lys Asp Ile Gly Ser Leu Gly
    15                  20                  25

agc aag gct tcg tct gtg tct gta aga cca agc cct cga act gag ggt   147
Ser Lys Ala Ser Ser Val Ser Val Arg Pro Ser Pro Arg Thr Glu Gly
30                  35                  40                  45

gag atc tta cag tct cca aat ctc aag agt ttt agc ttt gct gag ctt   195
Glu Ile Leu Gln Ser Pro Asn Leu Lys Ser Phe Ser Phe Ala Glu Leu
                50                  55                  60

aaa tca gca acc agg aat ttt aga cca gac agt gtg ctt ggt gaa ggt   243
Lys Ser Ala Thr Arg Asn Phe Arg Pro Asp Ser Val Leu Gly Glu Gly
            65                  70                  75

gga ttc ggt tgt gtt ttc aaa gga tgg att gat gag aag tct ctc act   291
Gly Phe Gly Cys Val Phe Lys Gly Trp Ile Asp Glu Lys Ser Leu Thr
        80                  85                  90

gcc tca aga cca ggc acg ggt ttg gtt att gcc gtc aaa aag ctt aac   339
Ala Ser Arg Pro Gly Thr Gly Leu Val Ile Ala Val Lys Lys Leu Asn
    95                  100                 105

caa gat ggt tgg caa ggt cac cag gag tgg ctg gct gaa gtg aat tac   387
Gln Asp Gly Trp Gln Gly His Gln Glu Trp Leu Ala Glu Val Asn Tyr
```

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110                 115                 120                 125

ctt ggt cag ttt tct cac cgt cac ctt gtg aag ctg att ggt tat tgc    435
Leu Gly Gln Phe Ser His Arg His Leu Val Lys Leu Ile Gly Tyr Cys
                130                 135                 140

cta gag gat gag cac cgt ctt ctt gtt tac gag ttc atg cct cgg ggt    483
Leu Glu Asp Glu His Arg Leu Leu Val Tyr Glu Phe Met Pro Arg Gly
            145                 150                 155

agc ttg gag aat cat ctt ttc agg aga ggt ttg tac ttc caa ccg tta    531
Ser Leu Glu Asn His Leu Phe Arg Arg Gly Leu Tyr Phe Gln Pro Leu
        160                 165                 170

tct tgg aaa ctt cgg ttg aaa gtt gct ctt ggt gct gca aag gga ctt    579
Ser Trp Lys Leu Arg Leu Lys Val Ala Leu Gly Ala Ala Lys Gly Leu
    175                 180                 185

gct ttt ctt cac agt tcc gag aca aga gtg ata tac cga gat ttc aag    627
Ala Phe Leu His Ser Ser Glu Thr Arg Val Ile Tyr Arg Asp Phe Lys
190                 195                 200                 205

act tct aat atc ctt ctt gac tcg gag tac aac gca aag ctt tct gat    675
Thr Ser Asn Ile Leu Leu Asp Ser Glu Tyr Asn Ala Lys Leu Ser Asp
                210                 215                 220

ttt ggg ttg gct aag gat ggg cca ata ggt gat aaa agt cat gtc tct    723
Phe Gly Leu Ala Lys Asp Gly Pro Ile Gly Asp Lys Ser His Val Ser
            225                 230                 235

aca cga gtc atg ggt aca cac gga tat gca gct cct gaa tac ctt gca    771
Thr Arg Val Met Gly Thr His Gly Tyr Ala Ala Pro Glu Tyr Leu Ala
        240                 245                 250

acc ggt cat cta aca aca aag agt gat gtc tat agc ttc ggg gtt gtc    819
Thr Gly His Leu Thr Thr Lys Ser Asp Val Tyr Ser Phe Gly Val Val
    255                 260                 265

ctt ctg gag ctg ttg tct ggt cgt cga gca gtg gac aag aac cgc cca    867
Leu Leu Glu Leu Leu Ser Gly Arg Arg Ala Val Asp Lys Asn Arg Pro
270                 275                 280                 285

tct gga gag agg aac ctt gtg gag tgg gct aaa cca tac ctc gta aac    915
Ser Gly Glu Arg Asn Leu Val Glu Trp Ala Lys Pro Tyr Leu Val Asn
                290                 295                 300

aaa aga aag ata ttc cga gtc att gat aat cgt ctt cag gac cag tac    963
Lys Arg Lys Ile Phe Arg Val Ile Asp Asn Arg Leu Gln Asp Gln Tyr
            305                 310                 315

tct atg gaa gaa gca tgt aaa gtg gct act ctg tct ctg aga tgt ctc    1011
Ser Met Glu Glu Ala Cys Lys Val Ala Thr Leu Ser Leu Arg Cys Leu
        320                 325                 330

acc aca gag att aag ctg aga cca aac atg agc gag gtt gtt tcg cac    1059
Thr Thr Glu Ile Lys Leu Arg Pro Asn Met Ser Glu Val Val Ser His
    335                 340                 345
```

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ctc gaa cac att cag tct tta aat gct gct ata gga gga aat atg gat    1107
Leu Glu His Ile Gln Ser Leu Asn Ala Ala Ile Gly Gly Asn Met Asp
350                 355                 360                 365

aaa aca gat aga aga atg cgt agg aga agt gac agt gtt gtc agc aaa    1155
Lys Thr Asp Arg Arg Met Arg Arg Arg Ser Asp Ser Val Val Ser Lys
                370                 375                 380

aaa gtg aat gca ggt ttt gct cga cag act gct gtt ggc agt aca gtt    1203
Lys Val Asn Ala Gly Phe Ala Arg Gln Thr Ala Val Gly Ser Thr Val
            385                 390                 395

gtt gct tat cct cgc cca tca gcc tcg cca ctg tat gtt tga            1245
Val Ala Tyr Pro Arg Pro Ser Ala Ser Pro Leu Tyr Val
        400                 405                 410

atagggttaa ac                                                      1257
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<212> PRT
<213> Arabidopsis thaliana

<400> 68

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Met Gly Ile Cys Leu Ser Ala Gln Val Lys Ala Glu Ser Ser Gly Ala
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Ser Thr Lys Tyr Asp Ala Lys Asp Ile Gly Ser Leu Gly Ser Lys Ala
            20                  25                  30

Ser Ser Val Ser Val Arg Pro Ser Pro Arg Thr Glu Gly Glu Ile Leu
        35                  40                  45

Gln Ser Pro Asn Leu Lys Ser Phe Ser Phe Ala Glu Leu Lys Ser Ala
    50                  55                  60

Thr Arg Asn Phe Arg Pro Asp Ser Val Leu Gly Glu Gly Gly Phe Gly
 65                  70                  75                  80

Cys Val Phe Lys Gly Trp Ile Asp Glu Lys Ser Leu Thr Ala Ser Arg
                 85                  90                  95

Pro Gly Thr Gly Leu Val Ile Ala Val Lys Lys Leu Asn Gln Asp Gly
            100                 105                 110

Trp Gln Gly His Gln Glu Trp Leu Ala Glu Val Asn Tyr Leu Gly Gln
        115                 120                 125

Phe Ser His Arg His Leu Val Lys Leu Ile Gly Tyr Cys Leu Glu Asp
    130                 135                 140

Glu His Arg Leu Leu Val Tyr Glu Phe Met Pro Arg Gly Ser Leu Glu
145                 150                 155                 160

Asn His Leu Phe Arg Arg Gly Leu Tyr Phe Gln Pro Leu Ser Trp Lys
```

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                    165                 170                 175

Leu Arg Leu Lys Val Ala Leu Gly Ala Ala Lys Gly Leu Ala Phe Leu
            180                 185                 190

His Ser Ser Glu Thr Arg Val Ile Tyr Arg Asp Phe Lys Thr Ser Asn
        195                 200                 205

Ile Leu Leu Asp Ser Glu Tyr Asn Ala Lys Leu Ser Asp Phe Gly Leu
    210                 215                 220

Ala Lys Asp Gly Pro Ile Gly Asp Lys Ser His Val Ser Thr Arg Val
225                 230                 235                 240

Met Gly Thr His Gly Tyr Ala Ala Pro Glu Tyr Leu Ala Thr Gly His
                245                 250                 255

Leu Thr Thr Lys Ser Asp Val Tyr Ser Phe Gly Val Val Leu Leu Glu
            260                 265                 270

Leu Leu Ser Gly Arg Arg Ala Val Asp Lys Asn Arg Pro Ser Gly Glu
        275                 280                 285

Arg Asn Leu Val Glu Trp Ala Lys Pro Tyr Leu Val Asn Lys Arg Lys
    290                 295                 300

Ile Phe Arg Val Ile Asp Asn Arg Leu Gln Asp Gln Tyr Ser Met Glu
305                 310                 315                 320

Glu Ala Cys Lys Val Ala Thr Leu Ser Leu Arg Cys Leu Thr Thr Glu
                325                 330                 335

Ile Lys Leu Arg Pro Asn Met Ser Glu Val Val Ser His Leu Glu His
            340                 345                 350

Ile Gln Ser Leu Asn Ala Ala Ile Gly Gly Asn Met Asp Lys Thr Asp
        355                 360                 365

Arg Arg Met Arg Arg Arg Ser Asp Ser Val Val Ser Lys Lys Val Asn
    370                 375                 380

Ala Gly Phe Ala Arg Gln Thr Ala Val Gly Ser Thr Val Val Ala Tyr
385                 390                 395                 400

Pro Arg Pro Ser Ala Ser Pro Leu Tyr Val
                405                 410
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<400> 69
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gacgcaaa atg cta gag aaa aaa tta gct gct gca gaa gtc tct gag gaa  110
         Met Leu Glu Lys Lys Leu Ala Ala Ala Glu Val Ser Glu Glu
           1               5                  10

gag caa aat aac ttg cta aag gat ttg gag atg aag gaa act gaa tat   158
Glu Gln Asn Asn Leu Leu Lys Asp Leu Glu Met Lys Glu Thr Glu Tyr
 15                  20                  25                  30

atg cgc cgt cag agg cat aaa atg gga gct gat gac ttt gag cca ttg   206
```

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Met Arg Arg Gln Arg His Lys Met Gly Ala Asp Asp Phe Glu Pro Leu
                35                  40                  45

aca atg att ggg aag ggt gca ttc gga gag gtaacatctc ttttatagat    256
Thr Met Ile Gly Lys Gly Ala Phe Gly Glu
            50                  55

catagtctgt tactctgttt tctcagcctc tcattggcat gcatcatctt gaaatgttct 316

ctgtgatgca tccttcttga aaggtcttct taggccattt tttttaccac agctaatttt 376

tcaaaaaagt atggcatgct aatttttctc tttctctttg cag gtt agg atc tgt  431
                                                Val Arg Ile Cys
                                                             60

agg gag aag gga aca ggc aat gtc tat gca atg aag aag ctt aag aaa  479
Arg Glu Lys Gly Thr Gly Asn Val Tyr Ala Met Lys Lys Leu Lys Lys
                65                  70                  75

tct gag atg ctt cgc aga ggc cag gta tttaaattcc ttcaagtggc        526
Ser Glu Met Leu Arg Arg Gly Gln Val
            80                  85

tttcgtttga catttgttta gttggttgat gtgaatgtgg aatctgattt tcag gtg  583
                                                            Val

gaa cat gta aaa gca gag aga aat tta ctt gca gaa gtt gat agc aat  631
Glu His Val Lys Ala Glu Arg Asn Leu Leu Ala Glu Val Asp Ser Asn
            90                  95                  100

tgc att gtc aaa ctg tat tgt tct ttc caa gat gaa gag tac ttg tat  679
Cys Ile Val Lys Leu Tyr Cys Ser Phe Gln Asp Glu Glu Tyr Leu Tyr
        105                 110                 115

ctc ata atg gag tat tta cct ggt ggg gat atg atg act tta ctt atg  727
Leu Ile Met Glu Tyr Leu Pro Gly Gly Asp Met Met Thr Leu Leu Met
    120                 125                 130

agg aaa gac acc ctc act gaa gac gag gcc agg ttt tat att ggg gaa  775
Arg Lys Asp Thr Leu Thr Glu Asp Glu Ala Arg Phe Tyr Ile Gly Glu
135                 140                 145                 150

act gtc ctg gct att gag tcc att cat aag cac aac tac att cac ag   822
Thr Val Leu Ala Ile Glu Ser Ile His Lys His Asn Tyr Ile His Ar
                155                 160                 165

gtcagtgaag cagaatatat gatttagttc tagctcccat tgttattttg ttctaaacgt 882

ctttttttct ccaatgtgat acag a gat atc aag cct gat aat ctg cta ctt  934
                          g Asp Ile Lys Pro Asp Asn Leu Leu Leu
                            s          170                 175

gac aaa gac ggc cac atg aaa ttg tca gat ttt gga tta tgt aaa cca  982
Asp Lys Asp Gly His Met Lys Leu Ser Asp Phe Gly Leu Cys Lys Pro
                180                 185                 190

tta gac tgt agt aat ctt caa gag aaa gac ttt aca gtt gca aga aac  1030
```

```
Leu Asp Cys Ser Asn Leu Gln Glu Lys Asp Phe Thr Val Ala Arg Asn
            195                 200                 205

gtt agt ggg gct tta caa agt gat ggt cgc cct gtg gcg aca aga cgc    1078
Val Ser Gly Ala Leu Gln Ser Asp Gly Arg Pro Val Ala Thr Arg Arg
        210                 215                 220

acc caa caa gag caa tta cta aac tgg cag aga aat aga agg atg ctt    1126
Thr Gln Gln Glu Gln Leu Leu Asn Trp Gln Arg Asn Arg Arg Met Leu
    225                 230                 235

gtaagtttca cttattcctc atcttttctt ccagagatgt ggagtagtcc acagtatcca 1186

gtatatttcg ttattgaaag caaattctct ccattgatat agacatctat gttagatatg 1246

acttactagg ttaaggtcat tactttcag gct tat tcc aca gtt ggc act cct    1299
                                Ala Tyr Ser Thr Val Gly Thr Pro
                                240                 245

gac tat att gcc cca gaa gtt ctg ttg aaa aaa gga tat gga atg gaa    1347
Asp Tyr Ile Ala Pro Glu Val Leu Leu Lys Lys Gly Tyr Gly Met Glu
        250                 255                 260

tgt gat tg gtaggtgaag ccaacctatt cctatttgtg gtctttgatt tctttggtgt 1405
Cys Asp Tr
    265

aaataaataa tatgggtgaa taatcttgag atttag g tgg tct ctt ggc gcc att 1460
                                        p Trp Ser Leu Gly Ala Ile
                                                      270

atg tat gaa atg ctt gtg ggg ttt ccg ccc ttt tat tca gat gac cca    1508
Met Tyr Glu Met Leu Val Gly Phe Pro Pro Phe Tyr Ser Asp Asp Pro
        275                 280                 285

atg aca act tgt agg aag gtaattaatc cattcctttt tgaatctttc           1556
Met Thr Thr Cys Arg Lys
    290

attttaatat tgaaggcaga ctggcgattt caagtcttac atttaatttt agtctttttg 1616

tatctctttg gtaattctaa tgtggaaact tacctcttct cgattcatta tcttccccct 1676

tatgcag ata gta aat tgg aga aat tac ttg aaa ttc cca gat gag gtt    1725
        Ile Val Asn Trp Arg Asn Tyr Leu Lys Phe Pro Asp Glu Val
        295                 300                 305

aga cta tca cca gaa gcc aag gat ctt att tgt agg ctt tta tgc aat    1773
Arg Leu Ser Pro Glu Ala Lys Asp Leu Ile Cys Arg Leu Leu Cys Asn
    310                 315                 320

gtt gaa caa agg ctt gga aca aaa gga gca gat gaa att aag            1815
Val Glu Gln Arg Leu Gly Thr Lys Gly Ala Asp Glu Ile Lys
325                 330                 335

gtgttgtatg cgttgttcaa ctttgagatt caaagttccc ttatgtaaga tcattgtgtg 1875
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caattcttaa aaacgatttg actggtttct ttcag ggt cac cct tgg ttt aga    1928
                                       Gly His Pro Trp Phe Arg
                                           340

ggc aca gaa tgg gga aaa ttg tat caa atg aaa gct gcc ttt att ccc   1976
Gly Thr Glu Trp Gly Lys Leu Tyr Gln Met Lys Ala Ala Phe Ile Pro
345                 350                 355                 360

caa gtt aat gat gag ttg gac acc caa aat ttt gag aaa ttt gaa gag   2024
Gln Val Asn Asp Glu Leu Asp Thr Gln Asn Phe Glu Lys Phe Glu Glu
                365                 370                 375

gtaacacact gatactatca gctaatgatg tctatagtga aatattggtg caatatatgc 2084

caccaaatga tgtggcatga tgtatatact gaaatattgg tatcacagat gatttttatg 2144

ctcctgataa ggaaaataat gtatactctt ctttgattcc ttctggaaca g act gac  2201
                                                         Thr Asp

aag caa gtt cca aag tca gcc aag tca ggt cca tgg aga aag           2243
Lys Gln Val Pro Lys Ser Ala Lys Ser Gly Pro Trp Arg Lys
    380                 385                 390

gtacagcata agcactgact ttttggcatt atgtaccatc aagctttttt tttttatcta 2303

atagaagagt gatcatactt caaaatttat ctataagtgg gttccttgag atatgttgtt 2363

ctttgatgat actacagacg tagcttaaaa tattacatgc aacaaagagc tcagaatgat 2423

gaaattggct cagtttctgt cacaggcgtt tctatctttg tactatattc acaaaaacgt 2483

gattcactct tttaggttca aattttctta tggtaattta gaatttggag ctgattggga 2543

tgctactaac agaattatgt tgttaatctg ccagttctgc atgttgacgt gtgttagatg 2603

aatcacttat ctttttggac caacatgata taacttagaa cctgttctgt caatagaatt 2663

tatgtcatga accaaaagga ttcttgtgaa tttcataaca tgacgctggc tttctttttt 2723

tcttctccag atg ctc tca tcc aaa gac att aac ttt gtt ggt tat act    2772
           Met Leu Ser Ser Lys Asp Ile Asn Phe Val Gly Tyr Thr
                   395                 400                 405

tac aag aac gta gaa atc gta aat gat gac caa ata cca ggg ata g     2818
Tyr Lys Asn Val Glu Ile Val Asn Asp Asp Gln Ile Pro Gly Ile A
                410                 415                 420

gtaattcact taacccccct tccgttgctg aggaagaagc aacaatacta gattaccttg 2878

tgattatcat cgcatgtttg ctgcatttgt aatttgtttt attgtgcag ct gag ttg  2935
                                                       la Glu Leu
                                                        G

aag aag aag agc aat aag cca aaa agg ccg tct att aaa tct ctc ttt g 2984
Lys Lys Lys Ser Asn Lys Pro Lys Arg Pro Ser Ile Lys Ser Leu Phe G
    425                 430                 435                 440
```

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gtaaatcatc tgtttgtatg ctatttgtaa aatcaagatg attacgatcc atgtttgatt 3044

ctctctaacc aaactgtgga aactaaatta acag aa gac gaa aca tct ggt ggg  3098
                                      lu Asp Glu Thr Ser Gly Gly
                                        A                445

aca aca acc cac caa gga agc ttt ttg aat cta cta ccg acg cag att   3146
Thr Thr Thr His Gln Gly Ser Phe Leu Asn Leu Leu Pro Thr Gln Ile
            450                 455                 460

gaa gat cca gag aaa gaa ggt agt aag tcg agc tca tcc ggg tga       3191
Glu Asp Pro Glu Lys Glu Gly Ser Lys Ser Ser Ser Ser Gly
        465                 470                 475

atttcatttg acacattgca cagcctgaac cagaagactc ttgttatat             3240


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<211> 476
<212> PRT
<213> Arabidopsis thaliana

<400> 70
Met Leu Glu Lys Lys Leu Ala Ala Ala Glu Val Ser Glu Glu Glu Gln
  1               5                  10                  15

Asn Asn Leu Leu Lys Asp Leu Glu Met Lys Glu Thr Glu Tyr Met Arg
             20                  25                  30

Arg Gln Arg His Lys Met Gly Ala Asp Asp Phe Glu Pro Leu Thr Met
         35                  40                  45

Ile Gly Lys Gly Ala Phe Gly Glu Val Arg Ile Cys Arg Glu Lys Gly
     50                  55                  60

Thr Gly Asn Val Tyr Ala Met Lys Lys Leu Lys Lys Ser Glu Met Leu
 65                  70                  75                  80

Arg Arg Gly Gln Val Val Glu His Val Lys Ala Glu Arg Asn Leu Leu
                 85                  90                  95

Ala Glu Val Asp Ser Asn Cys Ile Val Lys Leu Tyr Cys Ser Phe Gln
            100                 105                 110

Asp Glu Glu Tyr Leu Tyr Leu Ile Met Glu Tyr Leu Pro Gly Gly Asp
        115                 120                 125

Met Met Thr Leu Leu Met Arg Lys Asp Thr Leu Thr Glu Asp Glu Ala
    130                 135                 140

Arg Phe Tyr Ile Gly Glu Thr Val Leu Ala Ile Glu Ser Ile His Lys
145                 150                 155                 160

His Asn Tyr Ile His Arg Asp Ile Lys Pro Asp Asn Leu Leu Leu Asp
                165                 170                 175

Lys Asp Gly His Met Lys Leu Ser Asp Phe Gly Leu Cys Lys Pro Leu
```

180 185 190

Asp Cys Ser Asn Leu Gln Glu Lys Asp Phe Thr Val Ala Arg Asn Val
195 200 205

Ser Gly Ala Leu Gln Ser Asp Gly Arg Pro Val Ala Thr Arg Arg Thr
210 215 220

Gln Gln Glu Gln Leu Leu Asn Trp Gln Arg Asn Arg Arg Met Leu Ala
225 230 235 240

Tyr Ser Thr Val Gly Thr Pro Asp Tyr Ile Ala Pro Glu Val Leu Leu
245 250 255

Lys Lys Gly Tyr Gly Met Glu Cys Asp Trp Trp Ser Leu Gly Ala Ile
260 265 270

Met Tyr Glu Met Leu Val Gly Phe Pro Pro Phe Tyr Ser Asp Asp Pro
275 280 285

Met Thr Thr Cys Arg Lys Ile Val Asn Trp Arg Asn Tyr Leu Lys Phe
290 295 300

Pro Asp Glu Val Arg Leu Ser Pro Glu Ala Lys Asp Leu Ile Cys Arg
305 310 315 320

Leu Leu Cys Asn Val Glu Gln Arg Leu Gly Thr Lys Gly Ala Asp Glu
325 330 335

Ile Lys Gly His Pro Trp Phe Arg Gly Thr Glu Trp Gly Lys Leu Tyr
340 345 350

Gln Met Lys Ala Ala Phe Ile Pro Gln Val Asn Asp Glu Leu Asp Thr
355 360 365

Gln Asn Phe Glu Lys Phe Glu Glu Thr Asp Lys Gln Val Pro Lys Ser
370 375 380

Ala Lys Ser Gly Pro Trp Arg Lys Met Leu Ser Ser Lys Asp Ile Asn
385 390 395 400

Phe Val Gly Tyr Thr Tyr Lys Asn Val Glu Ile Val Asn Asp Asp Gln
405 410 415

Ile Pro Gly Ile Ala Glu Leu Lys Lys Lys Ser Asn Lys Pro Lys Arg
420 425 430

Pro Ser Ile Lys Ser Leu Phe Glu Asp Glu Thr Ser Gly Gly Thr Thr
435 440 445

Thr His Gln Gly Ser Phe Leu Asn Leu Leu Pro Thr Gln Ile Glu Asp
450 455 460

Pro Glu Lys Glu Gly Ser Lys Ser Ser Ser Ser Gly
465 470 475

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1 5

atg aac ggt gac gaa tgc gcg aac gtt gcg acg tgc tgg gtt act tct 102
Met Asn Gly Asp Glu Cys Ala Asn Val Ala Thr Cys Trp Val Thr Ser
10 15 20 25

cta gct tgt gta gtt gac gcc gga cga tat acg aaa aag gta tcc cac 150
Leu Ala Cys Val Val Asp Ala Gly Arg Tyr Thr Lys Lys Val Ser His
30 35 40

gac cgg cga acg agg tgg ccc gcc tgg aaa gca cga cgg gat cgt cat 198
Asp Arg Arg Thr Arg Trp Pro Ala Trp Lys Ala Arg Arg Asp Arg His
45 50 55

agt gtc cga agt gat agc ggc cta gac agt cat gca ctt gaa ggt gga 246
Ser Val Arg Ser Asp Ser Gly Leu Asp Ser His Ala Leu Glu Gly Gly
60 65 70

aaa cga cgt gag tca tgc gta tca cta gct cac gaa cga gat tat gca 294
Lys Arg Arg Glu Ser Cys Val Ser Leu Ala His Glu Arg Asp Tyr Ala
75 80 85

cta acg gca cgg tgg gat cgt agc att gca atg acg gat gac acg aac 342
Leu Thr Ala Arg Trp Asp Arg Ser Ile Ala Met Thr Asp Asp Thr Asn
90 95 100 105

cca caa acc caa cgt aaa ttt gag aaa cat act cgg gat gta gaa gct 390
Pro Gln Thr Gln Arg Lys Phe Glu Lys His Thr Arg Asp Val Glu Ala
110 115 120

gtt cga ttt tct cca cga gat cgt cta att gta tct gcg ggt gca gat 438
Val Arg Phe Ser Pro Arg Asp Arg Leu Ile Val Ser Ala Gly Ala Asp
125 130 135

ggg gta att gca gta tgt ccg gtt gct ggt gaa tgt gat gat gac gat 486
Gly Val Ile Ala Val Cys Pro Val Ala Gly Glu Cys Asp Asp Asp Asp
140 145 150

gcc cgt gat ggt cat gaa gat tgt gtt agt agt att tgc ttt tca cca 534
Ala Arg Asp Gly His Glu Asp Cys Val Ser Ser Ile Cys Phe Ser Pro
155 160 165

tca cta gaa cac ccg atc ctc ttt tct ggt agt tgt atc tac ttt att 582
Ser Leu Glu His Pro Ile Leu Phe Ser Gly Ser Cys Ile Tyr Phe Ile

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170                 175                 180                 185

aaa gtg tgg aat gtc aat gga aag aaa tgt agg acg ccg cta aaa aag     630
Lys Val Trp Asn Val Asn Gly Lys Lys Cys Arg Thr Pro Leu Lys Lys
                190                 195                 200

cat agt aat ccc gta tct aca cgg aca cag tca gaa gag gga agg cta     678
His Ser Asn Pro Val Ser Thr Arg Thr Gln Ser Glu Glu Gly Arg Leu
            205                 210                 215

tgt gca aaa ggt ggt aaa agc ggt gca cgg cta cta ccc gat cta agt     726
Cys Ala Lys Gly Gly Lys Ser Gly Ala Arg Leu Leu Pro Asp Leu Ser
        220                 225                 230

act cag gaa caa cta ccc aaa att aat caa gaa aac cct att aat caa     774
Thr Gln Glu Gln Leu Pro Lys Ile Asn Gln Glu Asn Pro Ile Asn Gln
    235                 240                 245

att gct ttt tca cct agt ccg ttc gtc gtc acg tgc caa acg gaa aga     822
Ile Ala Phe Ser Pro Ser Pro Phe Val Val Thr Cys Gln Thr Glu Arg
250                 255                 260                 265

tcc cta tct caa acg tgg tga ccgtgcaccg gcacggtgaa aaagtcgacc        873
Ser Leu Ser Gln Thr Trp
                270

ggatcgaccg accgaaagcc tgctcgctgg acaaaaaaag agctttttag gcctttcgct 933

ttttttgaag aaaaaaggct cgcgaaaaaa aaaaagctcg aaatca                  979


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<212> PRT
<213> Arabidopsis thaliana

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Met Ile Cys Arg Ile Arg Leu Gly Ser Met Asn Gly Asp Glu Cys Ala
  1               5                  10                  15

Asn Val Ala Thr Cys Trp Val Thr Ser Leu Ala Cys Val Val Asp Ala
            20                  25                  30

Gly Arg Tyr Thr Lys Lys Val Ser His Asp Arg Arg Thr Arg Trp Pro
        35                  40                  45

Ala Trp Lys Ala Arg Arg Asp Arg His Ser Val Arg Ser Asp Ser Gly
    50                  55                  60

Leu Asp Ser His Ala Leu Glu Gly Gly Lys Arg Arg Glu Ser Cys Val
65                  70                  75                  80

Ser Leu Ala His Glu Arg Asp Tyr Ala Leu Thr Ala Arg Trp Asp Arg
                85                  90                  95

Ser Ile Ala Met Thr Asp Asp Thr Asn Pro Gln Thr Gln Arg Lys Phe
            100                 105                 110
```

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Glu Lys His Thr Arg Asp Val Glu Ala Val Arg Phe Ser Pro Arg Asp
        115                 120                 125

Arg Leu Ile Val Ser Ala Gly Ala Asp Gly Val Ile Ala Val Cys Pro
    130                 135                 140

Val Ala Gly Glu Cys Asp Asp Asp Asp Ala Arg Asp Gly His Glu Asp
145                 150                 155                 160

Cys Val Ser Ser Ile Cys Phe Ser Pro Ser Leu Glu His Pro Ile Leu
                165                 170                 175

Phe Ser Gly Ser Cys Ile Tyr Phe Ile Lys Val Trp Asn Val Asn Gly
            180                 185                 190

Lys Lys Cys Arg Thr Pro Leu Lys Lys His Ser Asn Pro Val Ser Thr
        195                 200                 205

Arg Thr Gln Ser Glu Glu Gly Arg Leu Cys Ala Lys Gly Gly Lys Ser
    210                 215                 220

Gly Ala Arg Leu Leu Pro Asp Leu Ser Thr Gln Glu Gln Leu Pro Lys
225                 230                 235                 240

Ile Asn Gln Glu Asn Pro Ile Asn Gln Ile Ala Phe Ser Pro Ser Pro
                245                 250                 255

Phe Val Val Thr Cys Gln Thr Glu Arg Ser Leu Ser Gln Thr Trp
            260                 265                 270


<210> 73
<211> 1260
<212> DNA
<213> Arabidopsis thaliana

<220>
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<222> (101)..(155)

<220>
<221> CDS
<222> (254)..(660)

<220>
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<222> (750)..(1193)

<400> 73
gctcaattat gtttacaaca ttgttgtaat ttcaaaactt cataagaatt tctctgataa 60

taaagaaaaa gctggagtag aactatttta aagtgtcatc atg aag aga cta agc   115
                                            Met Lys Arg Leu Ser
                                            1               5
```

```
agc tca gat tca atg tgt ggt cta atc tcc act tct aca g gttcttatta  165
Ser Ser Asp Ser Met Cys Gly Leu Ile Ser Thr Ser Thr A
                10                  15

ccatctttgt tctttctact ttttgctaat gtcagacaaa acccatgtga tcctttcttc 225

actttccact gtttctttta ttgacaag at tca ttt ggt tac aca aca gat gaa 279
                               sp Ser Phe Gly Tyr Thr Thr Asp Glu
                                   20                  25

cag agt cca aga ggg tac gga agt aat tac caa tct atg ctt gaa ggt   327
Gln Ser Pro Arg Gly Tyr Gly Ser Asn Tyr Gln Ser Met Leu Glu Gly
        30                  35                  40

tac gat gaa gat gct aca cta atc gag gaa tat tcc ggc aac cac cac   375
Tyr Asp Glu Asp Ala Thr Leu Ile Glu Glu Tyr Ser Gly Asn His His
    45                  50                  55

cac atg ggt cta tcg gag aag aag aga aga tta aaa gtt gac caa gtc   423
His Met Gly Leu Ser Glu Lys Lys Arg Arg Leu Lys Val Asp Gln Val
 60                  65                  70                  75

aaa gct ctt gag aag aat ttc gaa ctt gag aat aaa ctc gaa cct gag   471
Lys Ala Leu Glu Lys Asn Phe Glu Leu Glu Asn Lys Leu Glu Pro Glu
                80                  85                  90

agg aaa act aaa tta gca caa gag ctt gga ctt caa cct cgt caa gta   519
Arg Lys Thr Lys Leu Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln Val
            95                 100                 105

gct gtt tgg ttt cag aac cgt cgt gca cgg tgg aaa aca aaa cag ctt   567
Ala Val Trp Phe Gln Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu
        110                 115                 120

gaa aaa gat tac ggt gtt ctt aag ggt caa tac gat tct ctc cgc cac   615
Glu Lys Asp Tyr Gly Val Leu Lys Gly Gln Tyr Asp Ser Leu Arg His
    125                 130                 135

aat ttc gat tct ctc cgc cgt gac aat gat tcc ctt ctc caa gag       660
Asn Phe Asp Ser Leu Arg Arg Asp Asn Asp Ser Leu Leu Gln Glu
140                 145                 150

gtacaatatt agagacttta aaccataaaa attgaaactt cagagacgaa aatgcaaaaa 720

ggtttgattt ttaaagtttt tggttgcag att agt aaa atc aaa gct aag gta    773
                                Ile Ser Lys Ile Lys Ala Lys Val
                                155                 160

aac ggt gaa gaa gat aac aac aac aac aaa gct att acg gag ggt gtt   821
Asn Gly Glu Glu Asp Asn Asn Asn Asn Lys Ala Ile Thr Glu Gly Val
        165                 170                 175

aag gaa gag gaa gtt cac aag acg gat tcg att cct tcg tct cct ctg   869
Lys Glu Glu Glu Val His Lys Thr Asp Ser Ile Pro Ser Ser Pro Leu
    180                 185                 190

cag ttt cta gaa cat tcc tct ggt ttt aac tac cgg cga agc ttc act   917
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Gln Phe Leu Glu His Ser Ser Gly Phe Asn Tyr Arg Arg Ser Phe Thr
195                 200                 205                 210

gac ctc cgt gac ctt cta ccg aat tcc acc gtt gtc gag gct gga tct     965
Asp Leu Arg Asp Leu Leu Pro Asn Ser Thr Val Val Glu Ala Gly Ser
                215                 220                 225

tcc gat agt tgc gat tca agc gcc gtt ctt aac gac gaa aca agt tct     1013
Ser Asp Ser Cys Asp Ser Ser Ala Val Leu Asn Asp Glu Thr Ser Ser
            230                 235                 240

gat aac gga aga ttg acg ccg cct gtg acg gtt act ggc ggg agt ttc     1061
Asp Asn Gly Arg Leu Thr Pro Pro Val Thr Val Thr Gly Gly Ser Phe
        245                 250                 255

tta cag ttt gtg aaa aca gag caa aca gag gat cac gag gat ttt cta     1109
Leu Gln Phe Val Lys Thr Glu Gln Thr Glu Asp His Glu Asp Phe Leu
    260                 265                 270

agc ggt gaa gaa gct tgt ggt ttc ttc tcc gat gaa cag ccg ccg tca     1157
Ser Gly Glu Glu Ala Cys Gly Phe Phe Ser Asp Glu Gln Pro Pro Ser
275                 280                 285                 290

ctt cat tgg tac tct gct tca gat cat tgg act tga gaattgttta          1203
Leu His Trp Tyr Ser Ala Ser Asp His Trp Thr
                295                 300

tcaaattggt gctctgttta gtctcaatgg gaaaacagag aagagggcaa aggtgga      1260


<210> 74
<211> 301
<212> PRT
<213> Arabidopsis thaliana

<400> 74
Met Lys Arg Leu Ser Ser Ser Asp Ser Met Cys Gly Leu Ile Ser Thr
  1               5                  10                  15

Ser Thr Asp Ser Phe Gly Tyr Thr Thr Asp Glu Gln Ser Pro Arg Gly
            20                  25                  30

Tyr Gly Ser Asn Tyr Gln Ser Met Leu Glu Gly Tyr Asp Glu Asp Ala
        35                  40                  45

Thr Leu Ile Glu Glu Tyr Ser Gly Asn His His His Met Gly Leu Ser
    50                  55                  60

Glu Lys Lys Arg Arg Leu Lys Val Asp Gln Val Lys Ala Leu Glu Lys
65                  70                  75                  80

Asn Phe Glu Leu Glu Asn Lys Leu Glu Pro Glu Arg Lys Thr Lys Leu
                85                  90                  95

Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln Val Ala Val Trp Phe Gln
            100                 105                 110
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Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu Glu Lys Asp Tyr Gly
        115                 120                 125

Val Leu Lys Gly Gln Tyr Asp Ser Leu Arg His Asn Phe Asp Ser Leu
    130                 135                 140

Arg Arg Asp Asn Asp Ser Leu Leu Gln Glu Ile Ser Lys Ile Lys Ala
145                 150                 155                 160

Lys Val Asn Gly Glu Glu Asp Asn Asn Asn Asn Lys Ala Ile Thr Glu
                165                 170                 175

Gly Val Lys Glu Glu Glu Val His Lys Thr Asp Ser Ile Pro Ser Ser
            180                 185                 190

Pro Leu Gln Phe Leu Glu His Ser Ser Gly Phe Asn Tyr Arg Arg Ser
        195                 200                 205

Phe Thr Asp Leu Arg Asp Leu Leu Pro Asn Ser Thr Val Val Glu Ala
    210                 215                 220

Gly Ser Ser Asp Ser Cys Asp Ser Ser Ala Val Leu Asn Asp Glu Thr
225                 230                 235                 240

Ser Ser Asp Asn Gly Arg Leu Thr Pro Pro Val Thr Val Thr Gly Gly
                245                 250                 255

Ser Phe Leu Gln Phe Val Lys Thr Glu Gln Thr Glu Asp His Glu Asp
            260                 265                 270

Phe Leu Ser Gly Glu Glu Ala Cys Gly Phe Phe Ser Asp Glu Gln Pro
        275                 280                 285

Pro Ser Leu His Trp Tyr Ser Ala Ser Asp His Trp Thr
    290                 295                 300


<210> 75
<211> 1122
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (22)..(1122)

<400> 75
acgtagctaa agtccgtttg a atg aac caa cgt gct gac cgt gac cgt gct      51
                        Met Asn Gln Arg Ala Asp Arg Asp Arg Ala
                          1               5                  10

agc tcg atc cgt tgg ttt gcc aac cga tta gtg agt ggt agc ctg tta      99
Ser Ser Ile Arg Trp Phe Ala Asn Arg Leu Val Ser Gly Ser Leu Leu
                 15                  20                  25

ttg tgt gct aac gcc tac agt cgt cgt act ccc gcg tcc ggg gcc gca     147
```

```
Leu Cys Ala Asn Ala Tyr Ser Arg Arg Thr Pro Ala Ser Gly Ala Ala
                30                  35                  40

tta cag cag atg aac cgt gcc agt cag tca gtg aat tac cga cga cgt     195
Leu Gln Gln Met Asn Arg Ala Ser Gln Ser Val Asn Tyr Arg Arg Arg
        45                  50                  55

gag ctg tca tta atc agc ggc cgg aaa cag ggt gtc cag tct ctg ggt     243
Glu Leu Ser Leu Ile Ser Gly Arg Lys Gln Gly Val Gln Ser Leu Gly
    60                  65                  70

tat aga ctt gca cgc ctc gat aac cgc gct ctt gca caa ttg ttg cac     291
Tyr Arg Leu Ala Arg Leu Asp Asn Arg Ala Leu Ala Gln Leu Leu His
75                  80                  85                  90

agg gat ggc cag ccc gag gaa gtg gta cag cgc ggc aat gaa atc agc     339
Arg Asp Gly Gln Pro Glu Glu Val Val Gln Arg Gly Asn Glu Ile Ser
                95                  100                 105

tat ttc gaa acg gga ctt gaa ccg acc acg ctt aga cgt gtg cgc gat     387
Tyr Phe Glu Thr Gly Leu Glu Pro Thr Thr Leu Arg Arg Val Arg Asp
            110                 115                 120

tgt gtt gtt gcc gct ctg cca acc gtt atc tat acc gga ttc aaa cgt     435
Cys Val Val Ala Ala Leu Pro Thr Val Ile Tyr Thr Gly Phe Lys Arg
        125                 130                 135

gtt tct cct tac tac gaa ttt atc tcc gtc ggg cgc acg agg gtt gct     483
Val Ser Pro Tyr Tyr Glu Phe Ile Ser Val Gly Arg Thr Arg Val Ala
    140                 145                 150

gat cgt ctt agc gaa gtc acg caa gtg gtt ccc cga gat gat aca cgc     531
Asp Arg Leu Ser Glu Val Thr Gln Val Val Pro Arg Asp Asp Thr Arg
155                 160                 165                 170

tac gtc tac atc gtg tgg cgg gaa tcc gaa cga tcg aaa tta gag gcg     579
Tyr Val Tyr Ile Val Trp Arg Glu Ser Glu Arg Ser Lys Leu Glu Ala
                175                 180                 185

cgg ggg gat ctc cgt gat cgc gat ggt gaa acg ctg gaa aag ttt cgc     627
Arg Gly Asp Leu Arg Asp Arg Asp Gly Glu Thr Leu Glu Lys Phe Arg
            190                 195                 200

gtg att gct ttt aac gtc acg ctg gat atc agc agc agt atg gag ccg     675
Val Ile Ala Phe Asn Val Thr Leu Asp Ile Ser Ser Ser Met Glu Pro
        205                 210                 215

ctg gcg aag gga gat ttg ccg ccg ttg ctt gct gtt cct gta ggt gaa     723
Leu Ala Lys Gly Asp Leu Pro Pro Leu Leu Ala Val Pro Val Gly Glu
    220                 225                 230

caa gct aga ttc agc ttg acg cca acc tgg ttg cca cag ggt cgt agc     771
Gln Ala Arg Phe Ser Leu Thr Pro Thr Trp Leu Pro Gln Gly Arg Ser
235                 240                 245                 250

gat gtt tcc agt agt cga cgt ggg cta ccg cgg atg gac aaa gtg cct     819
Asp Val Ser Ser Ser Arg Arg Gly Leu Pro Arg Met Asp Lys Val Pro
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                255                 260                 265

atc gaa tcc cgt ctc tcg acc gac gga gta ttc agc ttc tcg gta aac     867
Ile Glu Ser Arg Leu Ser Thr Asp Gly Val Phe Ser Phe Ser Val Asn
            270                 275                 280

gtt aac ggc gct acg cca tcg agg tgg gat cag atg ttg cgc acc gga     915
Val Asn Gly Ala Thr Pro Ser Arg Trp Asp Gln Met Leu Arg Thr Gly
        285                 290                 295

cgc agg ccc gtc agt aga agc gta cgt gat gtc gcc gaa aac acc att     963
Arg Arg Pro Val Ser Arg Ser Val Arg Asp Val Ala Glu Asn Thr Ile
    300                 305                 310

ggc ggt gaa ctg ccg ccg cgt agc tgc tcg cga ccc gat ccg ttg acc     1011
Gly Gly Glu Leu Pro Pro Arg Ser Cys Ser Arg Pro Asp Pro Leu Thr
315                 320                 325                 330

gct gac cgc cga cgc tgc gct agc ctg agc ctg ccc agc ctg cca gct     1059
Ala Asp Arg Arg Arg Cys Ala Ser Leu Ser Leu Pro Ser Leu Pro Ala
                335                 340                 345

cga cag ccc tcc caa acg gag aaa cgc att gtc gag aat att aag tac     1107
Arg Gln Pro Ser Gln Thr Glu Lys Arg Ile Val Glu Asn Ile Lys Tyr
            350                 355                 360

ggg gca gcg cca tga                                                 1122
Gly Ala Ala Pro
        365


<210> 76
<211> 366
<212> PRT
<213> Arabidopsis thaliana

<400> 76
Met Asn Gln Arg Ala Asp Arg Asp Arg Ala Ser Ser Ile Arg Trp Phe
  1               5                  10                  15

Ala Asn Arg Leu Val Ser Gly Ser Leu Leu Leu Cys Ala Asn Ala Tyr
            20                  25                  30

Ser Arg Arg Thr Pro Ala Ser Gly Ala Ala Leu Gln Gln Met Asn Arg
        35                  40                  45

Ala Ser Gln Ser Val Asn Tyr Arg Arg Arg Glu Leu Ser Leu Ile Ser
    50                  55                  60

Gly Arg Lys Gln Gly Val Gln Ser Leu Gly Tyr Arg Leu Ala Arg Leu
 65                  70                  75                  80

Asp Asn Arg Ala Leu Ala Gln Leu Leu His Arg Asp Gly Gln Pro Glu
                 85                  90                  95

Glu Val Val Gln Arg Gly Asn Glu Ile Ser Tyr Phe Glu Thr Gly Leu
            100                 105                 110
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Glu Pro Thr Thr Leu Arg Arg Val Arg Asp Cys Val Val Ala Ala Leu
        115                 120                 125

Pro Thr Val Ile Tyr Thr Gly Phe Lys Arg Val Ser Pro Tyr Tyr Glu
    130                 135                 140

Phe Ile Ser Val Gly Arg Thr Arg Val Ala Asp Arg Leu Ser Glu Val
145                 150                 155                 160

Thr Gln Val Val Pro Arg Asp Asp Thr Arg Tyr Val Tyr Ile Val Trp
                165                 170                 175

Arg Glu Ser Glu Arg Ser Lys Leu Glu Ala Arg Gly Asp Leu Arg Asp
            180                 185                 190

Arg Asp Gly Glu Thr Leu Glu Lys Phe Arg Val Ile Ala Phe Asn Val
        195                 200                 205

Thr Leu Asp Ile Ser Ser Ser Met Glu Pro Leu Ala Lys Gly Asp Leu
    210                 215                 220

Pro Pro Leu Leu Ala Val Pro Val Gly Glu Gln Ala Arg Phe Ser Leu
225                 230                 235                 240

Thr Pro Thr Trp Leu Pro Gln Gly Arg Ser Asp Val Ser Ser Ser Arg
                245                 250                 255

Arg Gly Leu Pro Arg Met Asp Lys Val Pro Ile Glu Ser Arg Leu Ser
            260                 265                 270

Thr Asp Gly Val Phe Ser Phe Ser Val Asn Val Asn Gly Ala Thr Pro
        275                 280                 285

Ser Arg Trp Asp Gln Met Leu Arg Thr Gly Arg Arg Pro Val Ser Arg
    290                 295                 300

Ser Val Arg Asp Val Ala Glu Asn Thr Ile Gly Gly Glu Leu Pro Pro
305                 310                 315                 320

Arg Ser Cys Ser Arg Pro Asp Pro Leu Thr Ala Asp Arg Arg Arg Cys
                325                 330                 335

Ala Ser Leu Ser Leu Pro Ser Leu Pro Ala Arg Gln Pro Ser Gln Thr
            340                 345                 350

Glu Lys Arg Ile Val Glu Asn Ile Lys Tyr Gly Ala Ala Pro
        355                 360                 365
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<210> 77
<211> 1650
<212> DNA
<213> Arabidopsis thaliana

<220>

<221> CDS
<222> (21)..(203)

<220>
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<222> (633)..(838)

<220>
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<222> (1044)..(1605)

<400> 77

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attcagagaa gaactcaccg atg agt atg gat ttt tca cct ttg tta acg gtt 53
                      Met Ser Met Asp Phe Ser Pro Leu Leu Thr Val
                      1               5                   10

ctt gag gga gat ttc aac aag gat aat act tct tct gca aca gaa att   101
Leu Glu Gly Asp Phe Asn Lys Asp Asn Thr Ser Ser Ala Thr Glu Ile
            15                  20                  25

gat act tta gag aac tta gat gac act agg cag ata agt aaa gga aaa   149
Asp Thr Leu Glu Asn Leu Asp Asp Thr Arg Gln Ile Ser Lys Gly Lys
        30                  35                  40

cct ccg agg cac ctc aca agc agt gct act agg ctg cag ctt gca gcc   197
Pro Pro Arg His Leu Thr Ser Ser Ala Thr Arg Leu Gln Leu Ala Ala
    45                  50                  55

aat gcg gtaatatact tgaccctgct ttttcttttt cctttttcttt gttacaatgg   253
Asn Ala
60

gattcgaatg atgtaactgg tttctgtttg tgcgcag gat gtg gat gtt tgt aac  308
                                        Asp Val Asp Val Cys Asn
                                                        65

ttg gtt atg aag tca ctt gat gac aaa tca gag ttt cta cct gta tac   356
Leu Val Met Lys Ser Leu Asp Asp Lys Ser Glu Phe Leu Pro Val Tyr
        70                  75                  80

cga tca gga agt tgt gct gag caa ggg gca aaa cag ttc atg gaa gat   404
Arg Ser Gly Ser Cys Ala Glu Gln Gly Ala Lys Gln Phe Met Glu Asp
    85                  90                  95

gaa cac att tgc atc gat gat ctt gtt aat cat ctt ggt gca gct att   452
Glu His Ile Cys Ile Asp Asp Leu Val Asn His Leu Gly Ala Ala Ile
100                 105                 110                 115

caa tgc tct tct ctt gga gcc ttc tat ggg gtgagtttat cttccaatct     502
Gln Cys Ser Ser Leu Gly Ala Phe Tyr Gly
                120                 125

tacccaaaga agcataaaag caattcacta gcctgattct tctttcttct cctcttttgt 562
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actagtacga tataagaggt attacttcaa aaactcttct aacatttgtt gattgtgtgt 622

cctttggcag gta ttt gat ggc cac ggt ggc aca gat gca gca cac ttt    671
           Val Phe Asp Gly His Gly Gly Thr Asp Ala Ala His Phe
                           130                 135

gtt aga aag aac att ctg aga ttc att gta gag gac tcc tcc ttc cca   719
Val Arg Lys Asn Ile Leu Arg Phe Ile Val Glu Asp Ser Ser Phe Pro
    140                 145                 150

cta tgc gta aag aaa gca att aag agt gct ttc tta aaa gct gat tat   767
Leu Cys Val Lys Lys Ala Ile Lys Ser Ala Phe Leu Lys Ala Asp Tyr
155                 160                 165                 170

gaa ttt gca gat gat tct tct ctt gac atc tct tct ggg acc act gcg   815
Glu Phe Ala Asp Asp Ser Ser Leu Asp Ile Ser Ser Gly Thr Thr Ala
                175                 180                 185

ctt aca gct ttt att ttt gga cg gtaagagcat ttaaattcgt atttatgaac   868
Leu Thr Ala Phe Ile Phe Gly Ar
            190

ttgggaagct atatatgtta tcacctgtat aatcatcaat acttatcagg ttgcctgtgt 928

gtataagata gagaataagg cttagtgtaa agacttatgt aacgggctgt tttaccatgt 988

ttctttgtag ttttgatgtg attttgaata gaattgctac tttctttctt tacag g    1044
                                                             g

agg ttg ata att gca aat gct ggt gat tgc cga gca gta ctg ggg aga   1092
Arg Leu Ile Ile Ala Asn Ala Gly Asp Cys Arg Ala Val Leu Gly Arg
195                 200                 205                 210

aga ggt agg gca att gag ttg tcc aaa gat cac aaa cca aac tgc aca   1140
Arg Gly Arg Ala Ile Glu Leu Ser Lys Asp His Lys Pro Asn Cys Thr
                215                 220                 225

gcc gag aaa gta aga ata gaa aag tta ggt gga gtt gtg tat gac ggt   1188
Ala Glu Lys Val Arg Ile Glu Lys Leu Gly Gly Val Val Tyr Asp Gly
            230                 235                 240

tac ctc aac ggg caa cta tca gtt gca cgt gcc att gga gac tgg cac   1236
Tyr Leu Asn Gly Gln Leu Ser Val Ala Arg Ala Ile Gly Asp Trp His
        245                 250                 255

atg aaa ggt ccc aaa ggc tct gct tgt ccg cta agc cca gag cca gag   1284
Met Lys Gly Pro Lys Gly Ser Ala Cys Pro Leu Ser Pro Glu Pro Glu
    260                 265                 270

ttg caa gag aca gac ctg agt gaa gac gac gag ttc ttg ata atg gga   1332
Leu Gln Glu Thr Asp Leu Ser Glu Asp Asp Glu Phe Leu Ile Met Gly
275                 280                 285                 290

tgt gat ggt ctg tgg gat gtg atg agc agc cag tgc gct gtg aca ata   1380
Cys Asp Gly Leu Trp Asp Val Met Ser Ser Gln Cys Ala Val Thr Ile
                295                 300                 305
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gct agg aag gaa ctg atg att cat aat gat cca gag aga tgc tct aga 1428
Ala Arg Lys Glu Leu Met Ile His Asn Asp Pro Glu Arg Cys Ser Arg
310 315 320

gag ctt gtg agg gag gcc ctt aaa cgg aat aca tgt gac aat ttg aca 1476
Glu Leu Val Arg Glu Ala Leu Lys Arg Asn Thr Cys Asp Asn Leu Thr
325 330 335

gtg att gtt gtg tgc ttc tct ccg gat cct cca cag agg ata gag atc 1524
Val Ile Val Val Cys Phe Ser Pro Asp Pro Pro Gln Arg Ile Glu Ile
340 345 350

cga atg cag tca cgg gtg agg cgg agc ata tct gcg gaa ggg tta aac 1572
Arg Met Gln Ser Arg Val Arg Arg Ser Ile Ser Ala Glu Gly Leu Asn
355 360 365 370

cta ctc aaa ggc gtg ctc gat ggc tat ccg tga gcatgttatg ttgtacgtta 1625
Leu Leu Lys Gly Val Leu Asp Gly Tyr Pro
375 380

ctttgtgaga ctattgccaa gttag 1650

<210> 78
<211> 380
<212> PRT
<213> Arabidopsis thaliana

<400> 78
Met Ser Met Asp Phe Ser Pro Leu Leu Thr Val Leu Glu Gly Asp Phe
1 5 10 15

Asn Lys Asp Asn Thr Ser Ser Ala Thr Glu Ile Asp Thr Leu Glu Asn
20 25 30

Leu Asp Asp Thr Arg Gln Ile Ser Lys Gly Lys Pro Pro Arg His Leu
35 40 45

Thr Ser Ser Ala Thr Arg Leu Gln Leu Ala Ala Asn Ala Asp Val Asp
50 55 60

Val Cys Asn Leu Val Met Lys Ser Leu Asp Asp Lys Ser Glu Phe Leu
65 70 75 80

Pro Val Tyr Arg Ser Gly Ser Cys Ala Glu Gln Gly Ala Lys Gln Phe
85 90 95

Met Glu Asp Glu His Ile Cys Ile Asp Asp Leu Val Asn His Leu Gly
100 105 110

Ala Ala Ile Gln Cys Ser Ser Leu Gly Ala Phe Tyr Gly Val Phe Asp
115 120 125

Gly His Gly Gly Thr Asp Ala Ala His Phe Val Arg Lys Asn Ile Leu
130 135 140

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Arg Phe Ile Val Glu Asp Ser Ser Phe Pro Leu Cys Val Lys Lys Ala
145                 150                 155                 160

Ile Lys Ser Ala Phe Leu Lys Ala Asp Tyr Glu Phe Ala Asp Asp Ser
                165                 170                 175

Ser Leu Asp Ile Ser Ser Gly Thr Thr Ala Leu Thr Ala Phe Ile Phe
            180                 185                 190

Gly Arg Arg Leu Ile Ile Ala Asn Ala Gly Asp Cys Arg Ala Val Leu
        195                 200                 205

Gly Arg Arg Gly Arg Ala Ile Glu Leu Ser Lys Asp His Lys Pro Asn
    210                 215                 220

Cys Thr Ala Glu Lys Val Arg Ile Glu Lys Leu Gly Gly Val Val Tyr
225                 230                 235                 240

Asp Gly Tyr Leu Asn Gly Gln Leu Ser Val Ala Arg Ala Ile Gly Asp
                245                 250                 255

Trp His Met Lys Gly Pro Lys Gly Ser Ala Cys Pro Leu Ser Pro Glu
            260                 265                 270

Pro Glu Leu Gln Glu Thr Asp Leu Ser Glu Asp Asp Glu Phe Leu Ile
        275                 280                 285

Met Gly Cys Asp Gly Leu Trp Asp Val Met Ser Ser Gln Cys Ala Val
    290                 295                 300

Thr Ile Ala Arg Lys Glu Leu Met Ile His Asn Asp Pro Glu Arg Cys
305                 310                 315                 320

Ser Arg Glu Leu Val Arg Glu Ala Leu Lys Arg Asn Thr Cys Asp Asn
                325                 330                 335

Leu Thr Val Ile Val Val Cys Phe Ser Pro Asp Pro Pro Gln Arg Ile
            340                 345                 350

Glu Ile Arg Met Gln Ser Arg Val Arg Arg Ser Ile Ser Ala Glu Gly
        355                 360                 365

Leu Asn Leu Leu Lys Gly Val Leu Asp Gly Tyr Pro
    370                 375                 380


<210> 79
<211> 589
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (18)..(575)

<400> 79
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atctttttcc gataact atg gct gag gaa atc aag aat gtt cct gaa cag      50
                   Met Ala Glu Glu Ile Lys Asn Val Pro Glu Gln
                     1               5                  10

gag gtg cca aag gta gca aca gag gaa tca tcg gca gag gtt aca gat     98
Glu Val Pro Lys Val Ala Thr Glu Glu Ser Ser Ala Glu Val Thr Asp
            15                  20                  25

cgt gga ttg ttc gat ttc ttg gga aag aag aaa gac gaa aca aaa cca    146
Arg Gly Leu Phe Asp Phe Leu Gly Lys Lys Lys Asp Glu Thr Lys Pro
        30                  35                  40

gag gag act ccg atc gct tca gag ttt gag cag aag gtt cat att tca    194
Glu Glu Thr Pro Ile Ala Ser Glu Phe Glu Gln Lys Val His Ile Ser
    45                  50                  55

gag ccg gag cca gag gtt aaa cac gaa agt ctt ctt gaa aag ctt cac    242
Glu Pro Glu Pro Glu Val Lys His Glu Ser Leu Leu Glu Lys Leu His
60                  65                  70                  75

cga agc gac agt tct tct agc tcc tca agt gag gaa gaa ggt tca gat    290
Arg Ser Asp Ser Ser Ser Ser Ser Ser Ser Glu Glu Glu Gly Ser Asp
                80                  85                  90

ggt gag aag agg aag aag aag aag gag aag aag aag cca act act gaa    338
Gly Glu Lys Arg Lys Lys Lys Lys Glu Lys Lys Lys Pro Thr Thr Glu
            95                  100                 105

gtt gag gta aag gag gaa gag aag aaa ggg ttt atg gag aag ttg aaa    386
Val Glu Val Lys Glu Glu Glu Lys Lys Gly Phe Met Glu Lys Leu Lys
        110                 115                 120

gag aag ctt cct gga cac aag aaa cct gaa gac ggt tca gcc gtc gct    434
Glu Lys Leu Pro Gly His Lys Lys Pro Glu Asp Gly Ser Ala Val Ala
    125                 130                 135

gcg gca ccg gtg gtt gtt cct cct cct gtg gaa gaa gcg cat cca gtg    482
Ala Ala Pro Val Val Val Pro Pro Pro Val Glu Glu Ala His Pro Val
140                 145                 150                 155

gag aag aaa ggg att ctt gag aag att aag gag aag ctt cca gga tac    530
Glu Lys Lys Gly Ile Leu Glu Lys Ile Lys Glu Lys Leu Pro Gly Tyr
                160                 165                 170

cac cct aag acc acc gta gag gag gag aag aaa gat aaa gaa taa        575
His Pro Lys Thr Thr Val Glu Glu Glu Lys Lys Asp Lys Glu
            175                 180                 185

gaagattatc attaa                                                   590
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<210> 80
<211> 185
<212> PRT
<213> Arabidopsis thaliana

<400> 80

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Met Ala Glu Glu Ile Lys Asn Val Pro Glu Gln Glu Val Pro Lys Val
 1               5                  10                  15

Ala Thr Glu Glu Ser Ser Ala Glu Val Thr Asp Arg Gly Leu Phe Asp
            20                  25                  30

Phe Leu Gly Lys Lys Lys Asp Glu Thr Lys Pro Glu Glu Thr Pro Ile
        35                  40                  45

Ala Ser Glu Phe Glu Gln Lys Val His Ile Ser Glu Pro Glu Pro Glu
    50                  55                  60

Val Lys His Glu Ser Leu Leu Glu Lys Leu His Arg Ser Asp Ser Ser
65                  70                  75                  80

Ser Ser Ser Ser Ser Glu Glu Glu Gly Ser Asp Gly Glu Lys Arg Lys
                85                  90                  95

Lys Lys Lys Glu Lys Lys Lys Pro Thr Thr Glu Val Glu Val Lys Glu
            100                 105                 110

Glu Glu Lys Lys Gly Phe Met Glu Lys Leu Lys Glu Lys Leu Pro Gly
        115                 120                 125

His Lys Lys Pro Glu Asp Gly Ser Ala Val Ala Ala Ala Pro Val Val
    130                 135                 140

Val Pro Pro Pro Val Glu Glu Ala His Pro Val Glu Lys Lys Gly Ile
145                 150                 155                 160

Leu Glu Lys Ile Lys Glu Lys Leu Pro Gly Tyr His Pro Lys Thr Thr
                165                 170                 175

Val Glu Glu Glu Lys Lys Asp Lys Glu
            180                 185


<210> 81
<211> 1376
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (20)..(1366)

<400> 81
agcaatcgag aaaaaagca atg gcg tca gac aaa caa aag gcg gag aga gcc   52
                     Met Ala Ser Asp Lys Gln Lys Ala Glu Arg Ala
                      1               5                  10

gag gtt gcg gcg agg cta gcg gct gag gac ttg cat gac att aac aaa   100
Glu Val Ala Ala Arg Leu Ala Ala Glu Asp Leu His Asp Ile Asn Lys
            15                  20                  25

tcc ggt ggt gct gat gtc aca atg tat aag gtg acg gag aga aca act   148
```

```
Ser Gly Gly Ala Asp Val Thr Met Tyr Lys Val Thr Glu Arg Thr Thr
         30                  35                  40

gaa cat cca ccg gag caa gat agg ccc ggt gtg ata ggt tca gtg ttc    196
Glu His Pro Pro Glu Gln Asp Arg Pro Gly Val Ile Gly Ser Val Phe
     45                  50                  55

agg gct gtc caa gga acg tat gag cat gcg aga gac gct gta gtt gga    244
Arg Ala Val Gln Gly Thr Tyr Glu His Ala Arg Asp Ala Val Val Gly
 60                  65                  70                  75

aaa acc cac gaa gcg gct gag tct acc aaa gaa gga gct cag ata gct    292
Lys Thr His Glu Ala Ala Glu Ser Thr Lys Glu Gly Ala Gln Ile Ala
                 80                  85                  90

tca gag aaa gcg gtt gga gca aag gac gca acc gtc gag aaa gct aag    340
Ser Glu Lys Ala Val Gly Ala Lys Asp Ala Thr Val Glu Lys Ala Lys
             95                 100                 105

gaa acc gct gat tat act gcg gag aag gtg ggt gag tat aaa gac tat    388
Glu Thr Ala Asp Tyr Thr Ala Glu Lys Val Gly Glu Tyr Lys Asp Tyr
        110                 115                 120

acg gtt gat aaa gct aaa gag gct aag gac aca act gca gag aag gcg    436
Thr Val Asp Lys Ala Lys Glu Ala Lys Asp Thr Thr Ala Glu Lys Ala
    125                 130                 135

aag gag act gct aat tat act gcg gat aag gcg gtg gaa gca aag gat    484
Lys Glu Thr Ala Asn Tyr Thr Ala Asp Lys Ala Val Glu Ala Lys Asp
140                 145                 150                 155

aag acg gcg gag aag att ggt gag tac aaa gac tat gcg gtg gat aag    532
Lys Thr Ala Glu Lys Ile Gly Glu Tyr Lys Asp Tyr Ala Val Asp Lys
                160                 165                 170

gca gta gaa gct aaa gat aag aca gcg gag aag gcg aag gag act tcg    580
Ala Val Glu Ala Lys Asp Lys Thr Ala Glu Lys Ala Lys Glu Thr Ser
            175                 180                 185

aat tat acg gcg gat aag gct aaa gag gct aag gac aag acg gct gag    628
Asn Tyr Thr Ala Asp Lys Ala Lys Glu Ala Lys Asp Lys Thr Ala Glu
        190                 195                 200

aag gtt ggt gag tat aag gat tac acg gtg gac aag gcc gtg gaa gct    676
Lys Val Gly Glu Tyr Lys Asp Tyr Thr Val Asp Lys Ala Val Glu Ala
    205                 210                 215

agg gat tac aca gcg gag aag gct att gaa gca aag gat aag aca gct    724
Arg Asp Tyr Thr Ala Glu Lys Ala Ile Glu Ala Lys Asp Lys Thr Ala
220                 225                 230                 235

gag aag act gga gag tat aag gac tat acg gtg gag aag gcg acg gag    772
Glu Lys Thr Gly Glu Tyr Lys Asp Tyr Thr Val Glu Lys Ala Thr Glu
                240                 245                 250

ggg aaa gat gtt acg gtg agt aag cta gga gag ctg aag gat agt gcc    820
Gly Lys Asp Val Thr Val Ser Lys Leu Gly Glu Leu Lys Asp Ser Ala
```

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            255                 260                 265

gtt gag aca gcg aag aga gct atg ggt ttc ttg tcg ggg aag aca gag     868
Val Glu Thr Ala Lys Arg Ala Met Gly Phe Leu Ser Gly Lys Thr Glu
        270                 275                 280

gag gcc aaa gga aaa gct gtg gag acc aaa gat act gcc aag gaa aac     916
Glu Ala Lys Gly Lys Ala Val Glu Thr Lys Asp Thr Ala Lys Glu Asn
    285                 290                 295

atg gag aaa gct gga gaa gta aca aga caa aag atg gag gaa atg aga     964
Met Glu Lys Ala Gly Glu Val Thr Arg Gln Lys Met Glu Glu Met Arg
300                 305                 310                 315

ttg gaa ggt aaa gag ctc aaa gaa gaa gct gga gca aaa gcc caa gag     1012
Leu Glu Gly Lys Glu Leu Lys Glu Glu Ala Gly Ala Lys Ala Gln Glu
                320                 325                 330

gca tct caa aag act agg gag agt act gag tcg gga gct caa aaa gcc     1060
Ala Ser Gln Lys Thr Arg Glu Ser Thr Glu Ser Gly Ala Gln Lys Ala
            335                 340                 345

gaa gag acc aaa gat tct cct gcc gtg agg gga aat gaa gcg aaa ggg     1108
Glu Glu Thr Lys Asp Ser Pro Ala Val Arg Gly Asn Glu Ala Lys Gly
        350                 355                 360

act att ttt ggt gca tta ggg aat gta acg gaa gca ata aag agc aaa     1156
Thr Ile Phe Gly Ala Leu Gly Asn Val Thr Glu Ala Ile Lys Ser Lys
    365                 370                 375

ctg aca atg cca tca gac att gtg gag gaa aca cgc gcg gca cgt gag     1204
Leu Thr Met Pro Ser Asp Ile Val Glu Glu Thr Arg Ala Ala Arg Glu
380                 385                 390                 395

cat gga ggg acg ggt agg act gtg gtt gaa gtc aag gtc gag gat tca     1252
His Gly Gly Thr Gly Arg Thr Val Val Glu Val Lys Val Glu Asp Ser
                400                 405                 410

aag ccg ggt aag gtg gcg act tca ctg aag gcg tcg gat caa atg acc     1300
Lys Pro Gly Lys Val Ala Thr Ser Leu Lys Ala Ser Asp Gln Met Thr
            415                 420                 425

ggt caa aca ttc aac gac gtt gga cgg atg gat gat gat gct cgg aaa     1348
Gly Gln Thr Phe Asn Asp Val Gly Arg Met Asp Asp Asp Ala Arg Lys
        430                 435                 440

gat aag gga aag ctg tga gaatactaga                                  1376
Asp Lys Gly Lys Leu
    445


<210> 82
<211> 448
<212> PRT
<213> Arabidopsis thaliana

<400> 82
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Met Ala Ser Asp Lys Gln Lys Ala Glu Arg Ala Glu Val Ala Ala Arg
1 5 10 15

Leu Ala Ala Glu Asp Leu His Asp Ile Asn Lys Ser Gly Gly Ala Asp
20 25 30

Val Thr Met Tyr Lys Val Thr Glu Arg Thr Thr Glu His Pro Pro Glu
35 40 45

Gln Asp Arg Pro Gly Val Ile Gly Ser Val Phe Arg Ala Val Gln Gly
50 55 60

Thr Tyr Glu His Ala Arg Asp Ala Val Val Gly Lys Thr His Glu Ala
65 70 75 80

Ala Glu Ser Thr Lys Glu Gly Ala Gln Ile Ala Ser Glu Lys Ala Val
85 90 95

Gly Ala Lys Asp Ala Thr Val Glu Lys Ala Lys Glu Thr Ala Asp Tyr
100 105 110

Thr Ala Glu Lys Val Gly Glu Tyr Lys Asp Tyr Thr Val Asp Lys Ala
115 120 125

Lys Glu Ala Lys Asp Thr Thr Ala Glu Lys Ala Lys Glu Thr Ala Asn
130 135 140

Tyr Thr Ala Asp Lys Ala Val Glu Ala Lys Asp Lys Thr Ala Glu Lys
145 150 155 160

Ile Gly Glu Tyr Lys Asp Tyr Ala Val Asp Lys Ala Val Glu Ala Lys
165 170 175

Asp Lys Thr Ala Glu Lys Ala Lys Glu Thr Ser Asn Tyr Thr Ala Asp
180 185 190

Lys Ala Lys Glu Ala Lys Asp Lys Thr Ala Glu Lys Val Gly Glu Tyr
195 200 205

Lys Asp Tyr Thr Val Asp Lys Ala Val Glu Ala Arg Asp Tyr Thr Ala
210 215 220

Glu Lys Ala Ile Glu Ala Lys Asp Lys Thr Ala Glu Lys Thr Gly Glu
225 230 235 240

Tyr Lys Asp Tyr Thr Val Glu Lys Ala Thr Glu Gly Lys Asp Val Thr
245 250 255

Val Ser Lys Leu Gly Glu Leu Lys Asp Ser Ala Val Glu Thr Ala Lys
260 265 270

Arg Ala Met Gly Phe Leu Ser Gly Lys Thr Glu Glu Ala Lys Gly Lys
275 280 285

Ala Val Glu Thr Lys Asp Thr Ala Lys Glu Asn Met Glu Lys Ala Gly
290 295 300

```
Glu Val Thr Arg Gln Lys Met Glu Glu Met Arg Leu Glu Gly Lys Glu
305                 310                 315                 320

Leu Lys Glu Glu Ala Gly Ala Lys Ala Gln Glu Ala Ser Gln Lys Thr
                325                 330                 335

Arg Glu Ser Thr Glu Ser Gly Ala Gln Lys Ala Glu Glu Thr Lys Asp
            340                 345                 350

Ser Pro Ala Val Arg Gly Asn Glu Ala Lys Gly Thr Ile Phe Gly Ala
        355                 360                 365

Leu Gly Asn Val Thr Glu Ala Ile Lys Ser Lys Leu Thr Met Pro Ser
    370                 375                 380

Asp Ile Val Glu Glu Thr Arg Ala Ala Arg Glu His Gly Gly Thr Gly
385                 390                 395                 400

Arg Thr Val Val Glu Val Lys Val Glu Asp Ser Lys Pro Gly Lys Val
                405                 410                 415

Ala Thr Ser Leu Lys Ala Ser Asp Gln Met Thr Gly Gln Thr Phe Asn
            420                 425                 430

Asp Val Gly Arg Met Asp Asp Asp Ala Arg Lys Asp Lys Gly Lys Leu
        435                 440                 445


&lt;210&gt; 83
&lt;211&gt; 561
&lt;212&gt; DNA
&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; (18)..(548)

&lt;400&gt; 83
aaccacacaa atacaaa atg aat gaa atg tcg ttc ttt ggt tat agt ttc      50
                   Met Asn Glu Met Ser Phe Phe Gly Tyr Ser Phe
                   1               5                   10

atc gta gta gca tta ttc ttc gat tta act caa gcc tat cgt cac act      98
Ile Val Val Ala Leu Phe Phe Asp Leu Thr Gln Ala Tyr Arg His Thr
            15                  20                  25

ccc gct caa ccg cca aaa gca aac gca aac ggt gat gtc aaa ccg caa     146
Pro Ala Gln Pro Pro Lys Ala Asn Ala Asn Gly Asp Val Lys Pro Gln
        30                  35                  40

gaa acg ctc gtg gtt cac aac aag gcc cga gcc atg gtc gga gtc gga     194
Glu Thr Leu Val Val His Asn Lys Ala Arg Ala Met Val Gly Val Gly
    45                  50                  55

cca atg gtg tgg aac gaa act ctt gcg acc tat gca cag agc tac gca     242
Pro Met Val Trp Asn Glu Thr Leu Ala Thr Tyr Ala Gln Ser Tyr Ala
```

```
60                  65                  70                  75

cat gaa cga gcc aga gac tgt gcc atg aag cat tcc ttg gga cca ttc    290
His Glu Arg Ala Arg Asp Cys Ala Met Lys His Ser Leu Gly Pro Phe
                80                  85                  90

ggc gag aat cta gcc gcg ggt tgg gga acg atg agc ggt ccg gta gca    338
Gly Glu Asn Leu Ala Ala Gly Trp Gly Thr Met Ser Gly Pro Val Ala
            95                  100                 105

act gag tat tgg atg acg gag aag gaa aat tac gat tat gat agt aac    386
Thr Glu Tyr Trp Met Thr Glu Lys Glu Asn Tyr Asp Tyr Asp Ser Asn
        110                 115                 120

acg tgt ggt ggt gat ggt gtg tgt gga cac tac act cag atc gtg tgg    434
Thr Cys Gly Gly Asp Gly Val Cys Gly His Tyr Thr Gln Ile Val Trp
    125                 130                 135

cgt gac tcg gtt cga ctt ggt tgt gcc tcc gtg aga tgt aag aat gat    482
Arg Asp Ser Val Arg Leu Gly Cys Ala Ser Val Arg Cys Lys Asn Asp
140                 145                 150                 155

gag tat att tgg gtg att tgt agc tat gat cct ccg ggg aat tac atc    530
Glu Tyr Ile Trp Val Ile Cys Ser Tyr Asp Pro Pro Gly Asn Tyr Ile
                160                 165                 170

ggt caa cgt cca tat tag tgattggatt tta                             561
Gly Gln Arg Pro Tyr
            175


<210> 84
<211> 176
<212> PRT
<213> Arabidopsis thaliana

<400> 84
Met Asn Glu Met Ser Phe Phe Gly Tyr Ser Phe Ile Val Val Ala Leu
1               5                   10                  15

Phe Phe Asp Leu Thr Gln Ala Tyr Arg His Thr Pro Ala Gln Pro Pro
            20                  25                  30

Lys Ala Asn Ala Asn Gly Asp Val Lys Pro Gln Glu Thr Leu Val Val
        35                  40                  45

His Asn Lys Ala Arg Ala Met Val Gly Val Gly Pro Met Val Trp Asn
    50                  55                  60

Glu Thr Leu Ala Thr Tyr Ala Gln Ser Tyr Ala His Glu Arg Ala Arg
65                  70                  75                  80

Asp Cys Ala Met Lys His Ser Leu Gly Pro Phe Gly Glu Asn Leu Ala
                85                  90                  95

Ala Gly Trp Gly Thr Met Ser Gly Pro Val Ala Thr Glu Tyr Trp Met
            100                 105                 110
```

```
Thr Glu Lys Glu Asn Tyr Asp Tyr Asp Ser Asn Thr Cys Gly Gly Asp
        115                 120                 125

Gly Val Cys Gly His Tyr Thr Gln Ile Val Trp Arg Asp Ser Val Arg
    130                 135                 140

Leu Gly Cys Ala Ser Val Arg Cys Lys Asn Asp Glu Tyr Ile Trp Val
145                 150                 155                 160

Ile Cys Ser Tyr Asp Pro Pro Gly Asn Tyr Ile Gly Gln Arg Pro Tyr
                165                 170                 175


<210> 85
<211> 988
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (12)..(977)

<400> 85
tttttaagaa a atg gca gct tct aag cga cta gtt gtc tct tgc ttg ttc   50
             Met Ala Ala Ser Lys Arg Leu Val Val Ser Cys Leu Phe
               1               5                  10

tta gtt ttg ttg ttt gct caa gcc aat tcg caa ggt ttg aaa gta ggt    98
Leu Val Leu Leu Phe Ala Gln Ala Asn Ser Gln Gly Leu Lys Val Gly
     15                  20                  25

ttc tac agc aaa aca tgc cca caa ctc gag ggt ata gtt aaa aag gtc   146
Phe Tyr Ser Lys Thr Cys Pro Gln Leu Glu Gly Ile Val Lys Lys Val
 30                  35                  40                  45

gtg ttc gat gcg atg aac aaa gca cca aca ctt ggt gct cct ttg ctt   194
Val Phe Asp Ala Met Asn Lys Ala Pro Thr Leu Gly Ala Pro Leu Leu
                 50                  55                  60

aga atg ttc ttc cac gac tgc ttc gtt cgg gga tgt gac gga tca gtt   242
Arg Met Phe Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val
             65                  70                  75

ttg tta gat aaa cca aac aat caa ggt gag aag agt gca gtt cct aac   290
Leu Leu Asp Lys Pro Asn Asn Gln Gly Glu Lys Ser Ala Val Pro Asn
         80                  85                  90

cta agt ctt cga ggg ttt ggc atc ata gac gat tcc aag gcg gct cta   338
Leu Ser Leu Arg Gly Phe Gly Ile Ile Asp Asp Ser Lys Ala Ala Leu
     95                 100                 105

gaa aaa gtg tgt ccg gga att gtt tct tgc tct gat atc ttg gca ctt   386
Glu Lys Val Cys Pro Gly Ile Val Ser Cys Ser Asp Ile Leu Ala Leu
110                 115                 120                 125
```

```
gtc gct aga gac gca atg gtt gca ctt gaa gga cca tca tgg gaa gtt     434
Val Ala Arg Asp Ala Met Val Ala Leu Glu Gly Pro Ser Trp Glu Val
                130                 135                 140

gaa acg gga aga aga gac ggt agg gtt tct aac atc aac gaa gtc aac     482
Glu Thr Gly Arg Arg Asp Gly Arg Val Ser Asn Ile Asn Glu Val Asn
            145                 150                 155

ttg cca tca cct ttt gat aac atc acc aag ctt atc agc gat ttt cgc     530
Leu Pro Ser Pro Phe Asp Asn Ile Thr Lys Leu Ile Ser Asp Phe Arg
        160                 165                 170

tca aag ggc ctc aac gag aag gat cta gtc att ctc tcg ggt ggt cac     578
Ser Lys Gly Leu Asn Glu Lys Asp Leu Val Ile Leu Ser Gly Gly His
    175                 180                 185

aca att gga atg gga cat tgt cct tta ttg aca aac cgg ctt tac aac     626
Thr Ile Gly Met Gly His Cys Pro Leu Leu Thr Asn Arg Leu Tyr Asn
190                 195                 200                 205

ttc acc gga aaa gga gac agc gac cca agt ttg gac tcg gag tac gcc     674
Phe Thr Gly Lys Gly Asp Ser Asp Pro Ser Leu Asp Ser Glu Tyr Ala
                210                 215                 220

gct aag ctc agg aag aaa tgc aag ccc acc gat acg acg acg gct cta     722
Ala Lys Leu Arg Lys Lys Cys Lys Pro Thr Asp Thr Thr Thr Ala Leu
            225                 230                 235

gag atg gat ccg ggg agt ttc aaa aca ttt gac ttg agc tac ttc acg     770
Glu Met Asp Pro Gly Ser Phe Lys Thr Phe Asp Leu Ser Tyr Phe Thr
        240                 245                 250

cta gtg gct aag aga aga gga ctt ttc cag tcg gat gct gct cta ctc     818
Leu Val Ala Lys Arg Arg Gly Leu Phe Gln Ser Asp Ala Ala Leu Leu
    255                 260                 265

gac aac tcc aag act agg gct tat gtc ttg caa cag ata aga act cat     866
Asp Asn Ser Lys Thr Arg Ala Tyr Val Leu Gln Gln Ile Arg Thr His
270                 275                 280                 285

ggg tca atg ttc ttt aac gac ttt ggt gtc tct atg gtg aaa atg ggt     914
Gly Ser Met Phe Phe Asn Asp Phe Gly Val Ser Met Val Lys Met Gly
                290                 295                 300

cgg act gga gtt ctt acg ggt aag gcc ggg gag atc cgt aag acg tgt     962
Arg Thr Gly Val Leu Thr Gly Lys Ala Gly Glu Ile Arg Lys Thr Cys
            305                 310                 315

cgg tct gct aat taa gagatataga aa                                   989
Arg Ser Ala Asn
        320
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<210> 86
<211> 321
<212> PRT
<213> Arabidopsis thaliana

<400> 86

Met Ala Ala Ser Lys Arg Leu Val Val Ser Cys Leu Phe Leu Val Leu
1 5 10 15

Leu Phe Ala Gln Ala Asn Ser Gln Gly Leu Lys Val Gly Phe Tyr Ser
20 25 30

Lys Thr Cys Pro Gln Leu Glu Gly Ile Val Lys Lys Val Val Phe Asp
35 40 45

Ala Met Asn Lys Ala Pro Thr Leu Gly Ala Pro Leu Leu Arg Met Phe
50 55 60

Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val Leu Leu Asp
65 70 75 80

Lys Pro Asn Asn Gln Gly Glu Lys Ser Ala Val Pro Asn Leu Ser Leu
85 90 95

Arg Gly Phe Gly Ile Ile Asp Asp Ser Lys Ala Ala Leu Glu Lys Val
100 105 110

Cys Pro Gly Ile Val Ser Cys Ser Asp Ile Leu Ala Leu Val Ala Arg
115 120 125

Asp Ala Met Val Ala Leu Glu Gly Pro Ser Trp Glu Val Glu Thr Gly
130 135 140

Arg Arg Asp Gly Arg Val Ser Asn Ile Asn Glu Val Asn Leu Pro Ser
145 150 155 160

Pro Phe Asp Asn Ile Thr Lys Leu Ile Ser Asp Phe Arg Ser Lys Gly
165 170 175

Leu Asn Glu Lys Asp Leu Val Ile Leu Ser Gly Gly His Thr Ile Gly
180 185 190

Met Gly His Cys Pro Leu Leu Thr Asn Arg Leu Tyr Asn Phe Thr Gly
195 200 205

Lys Gly Asp Ser Asp Pro Ser Leu Asp Ser Glu Tyr Ala Ala Lys Leu
210 215 220

Arg Lys Lys Cys Lys Pro Thr Asp Thr Thr Thr Ala Leu Glu Met Asp
225 230 235 240

Pro Gly Ser Phe Lys Thr Phe Asp Leu Ser Tyr Phe Thr Leu Val Ala
245 250 255

Lys Arg Arg Gly Leu Phe Gln Ser Asp Ala Ala Leu Leu Asp Asn Ser
260 265 270

Lys Thr Arg Ala Tyr Val Leu Gln Gln Ile Arg Thr His Gly Ser Met
275 280 285

Phe Phe Asn Asp Phe Gly Val Ser Met Val Lys Met Gly Arg Thr Gly

```
    290                 295                 300

Val Leu Thr Gly Lys Ala Gly Glu Ile Arg Lys Thr Cys Arg Ser Ala
305                 310                 315                 320

Asn



<210> 87
<211> 650
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (8)..(634)

<400> 87
agcgaca atg gcg tcg att acg aac ctc gcc tct tct ctc tct tca ctc      49
        Met Ala Ser Ile Thr Asn Leu Ala Ser Ser Leu Ser Ser Leu
          1               5                  10

tcg ttc tcc tcc caa gtt tct caa aga cct aac acc att tcc ttc ccc      97
Ser Phe Ser Ser Gln Val Ser Gln Arg Pro Asn Thr Ile Ser Phe Pro
 15                  20                  25                  30

cgc gcg aat tca gta ttc gca tta ccg gcg aaa tcc gca cgc cgc gct     145
Arg Ala Asn Ser Val Phe Ala Leu Pro Ala Lys Ser Ala Arg Arg Ala
                 35                  40                  45

tct cta tct atc acc gcc acg gta tct gct cca ccg gag gag gag gag     193
Ser Leu Ser Ile Thr Ala Thr Val Ser Ala Pro Pro Glu Glu Glu Glu
             50                  55                  60

ata gtt gaa ctg aag aaa tac gtc aaa tcg agg ctt ccc gga gga ttt     241
Ile Val Glu Leu Lys Lys Tyr Val Lys Ser Arg Leu Pro Gly Gly Phe
         65                  70                  75

gct gct cag aag att att ggc act gga cga cgt aag tgc gca atc gct     289
Ala Ala Gln Lys Ile Ile Gly Thr Gly Arg Arg Lys Cys Ala Ile Ala
     80                  85                  90

aga gtt gtt ctt cag gaa ggt act ggg aag gtt atc atc aac tat cgt     337
Arg Val Val Leu Gln Glu Gly Thr Gly Lys Val Ile Ile Asn Tyr Arg
 95                 100                 105                 110

gat gcc aag gag tac ctt cag gga aat cca ttg tgg ctt cag tat gtt     385
Asp Ala Lys Glu Tyr Leu Gln Gly Asn Pro Leu Trp Leu Gln Tyr Val
                115                 120                 125

aaa gta cca ttg gtg act tta gga tat gag aat agc tac gac ata ttt     433
Lys Val Pro Leu Val Thr Leu Gly Tyr Glu Asn Ser Tyr Asp Ile Phe
            130                 135                 140

gtg aaa gcc cat gga ggc ggt ctc tca ggt caa gct caa gca att acc     481
Val Lys Ala His Gly Gly Gly Leu Ser Gly Gln Ala Gln Ala Ile Thr
```

145 150 155

ttg gga gtc gca cgt gca ctc ctg aag gta agt gca gac cac aga tcg 529
Leu Gly Val Ala Arg Ala Leu Leu Lys Val Ser Ala Asp His Arg Ser
160 165 170

cct ttg aag aag gaa ggt ttg ctc act aga gat gcg aga gtg gtt gaa 577
Pro Leu Lys Lys Glu Gly Leu Leu Thr Arg Asp Ala Arg Val Val Glu
175 180 185 190

aga aag aag gcc ggg ctc aag aag gcg cgt aaa gcc cca caa ttc tcc 625
Arg Lys Lys Ala Gly Leu Lys Lys Ala Arg Lys Ala Pro Gln Phe Ser
195 200 205

aag cgt taa gagttttata tatcat 650
Lys Arg

<210> 88
<211> 208
<212> PRT
<213> Arabidopsis thaliana

<400> 88
Met Ala Ser Ile Thr Asn Leu Ala Ser Ser Leu Ser Ser Leu Ser Phe
1 5 10 15

Ser Ser Gln Val Ser Gln Arg Pro Asn Thr Ile Ser Phe Pro Arg Ala
20 25 30

Asn Ser Val Phe Ala Leu Pro Ala Lys Ser Ala Arg Arg Ala Ser Leu
35 40 45

Ser Ile Thr Ala Thr Val Ser Ala Pro Pro Glu Glu Glu Glu Ile Val
50 55 60

Glu Leu Lys Lys Tyr Val Lys Ser Arg Leu Pro Gly Gly Phe Ala Ala
65 70 75 80

Gln Lys Ile Ile Gly Thr Gly Arg Arg Lys Cys Ala Ile Ala Arg Val
85 90 95

Val Leu Gln Glu Gly Thr Gly Lys Val Ile Ile Asn Tyr Arg Asp Ala
100 105 110

Lys Glu Tyr Leu Gln Gly Asn Pro Leu Trp Leu Gln Tyr Val Lys Val
115 120 125

Pro Leu Val Thr Leu Gly Tyr Glu Asn Ser Tyr Asp Ile Phe Val Lys
130 135 140

Ala His Gly Gly Gly Leu Ser Gly Gln Ala Gln Ala Ile Thr Leu Gly
145 150 155 160

Val Ala Arg Ala Leu Leu Lys Val Ser Ala Asp His Arg Ser Pro Leu
165 170 175

```
Lys Lys Glu Gly Leu Leu Thr Arg Asp Ala Arg Val Val Glu Arg Lys
        180                 185                 190

Lys Ala Gly Leu Lys Lys Ala Arg Lys Ala Pro Gln Phe Ser Lys Arg
    195                 200                 205



<210> 89
<211> 1223
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (16)..(1215)

<400> 89
aacaagtgaa gcaca atg ggg atc atc gaa agg att aaa gaa atc gag gcc   51
                 Met Gly Ile Ile Glu Arg Ile Lys Glu Ile Glu Ala
                   1               5                  10

gag atg gct cgg act cag aag aat aaa gct aca gag tat cat ctt ggt    99
Glu Met Ala Arg Thr Gln Lys Asn Lys Ala Thr Glu Tyr His Leu Gly
         15                  20                  25

cag ctc aag gca aag att gca aaa ctc agg aca caa ctg ttg gag cct   147
Gln Leu Lys Ala Lys Ile Ala Lys Leu Arg Thr Gln Leu Leu Glu Pro
     30                  35                  40

cca aaa ggt gct agt gga ggc ggg gaa ggt ttt gaa gtt acc aag tat   195
Pro Lys Gly Ala Ser Gly Gly Gly Glu Gly Phe Glu Val Thr Lys Tyr
 45                  50                  55                  60

ggt cat gga cgt gtt gca ctt ata gga ttt cct agt gtc gga aag tcc   243
Gly His Gly Arg Val Ala Leu Ile Gly Phe Pro Ser Val Gly Lys Ser
                 65                  70                  75

acg ctt ttg act atg tta act gga aca cat tct gaa gca gcc tca tat   291
Thr Leu Leu Thr Met Leu Thr Gly Thr His Ser Glu Ala Ala Ser Tyr
             80                  85                  90

gaa ttt aca aca ctt aca tgc atc cct ggt gta att cac tac aac gac   339
Glu Phe Thr Thr Leu Thr Cys Ile Pro Gly Val Ile His Tyr Asn Asp
         95                 100                 105

aca aag att cag ctt ctc gat ctt cct ggg att att gaa ggt gct tcg   387
Thr Lys Ile Gln Leu Leu Asp Leu Pro Gly Ile Ile Glu Gly Ala Ser
    110                 115                 120

gaa gga aag ggg cga gga agg cag gtt att gct gtt gca aag tct tcc   435
Glu Gly Lys Gly Arg Gly Arg Gln Val Ile Ala Val Ala Lys Ser Ser
125                 130                 135                 140

gac ctt gta ttg atg gtt ctt gat gcc tca aaa agc gaa ggc cac agg   483
Asp Leu Val Leu Met Val Leu Asp Ala Ser Lys Ser Glu Gly His Arg
                145                 150                 155
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caa ata ttg act aag gaa ctt gag gca gtg ggc ttg cga cta aac aaa    531
Gln Ile Leu Thr Lys Glu Leu Glu Ala Val Gly Leu Arg Leu Asn Lys
            160                 165                 170

act cct ccg cag ata tac ttt aaa aag aaa aag act ggt gga atc tct    579
Thr Pro Pro Gln Ile Tyr Phe Lys Lys Lys Lys Thr Gly Gly Ile Ser
        175                 180                 185

ttc aac act aca gca ccc ttg act cac att gat gag aag ctc tgt tat    627
Phe Asn Thr Thr Ala Pro Leu Thr His Ile Asp Glu Lys Leu Cys Tyr
    190                 195                 200

caa atc ctg cat gaa tac aag att cac aat gct gag gtg cta ttt cgt    675
Gln Ile Leu His Glu Tyr Lys Ile His Asn Ala Glu Val Leu Phe Arg
205                 210                 215                 220

gag aat gcc aca gtg gat gac ttt att gat gtc att gaa ggc aac cgc    723
Glu Asn Ala Thr Val Asp Asp Phe Ile Asp Val Ile Glu Gly Asn Arg
                225                 230                 235

aag tat att aag tgt gtt tat gtc tac atc aaa ata gat gtt gtt gga    771
Lys Tyr Ile Lys Cys Val Tyr Val Tyr Ile Lys Ile Asp Val Val Gly
            240                 245                 250

att gat gat gtg gat aga cta tcc cgg cag cca aat tcc att gtt att    819
Ile Asp Asp Val Asp Arg Leu Ser Arg Gln Pro Asn Ser Ile Val Ile
        255                 260                 265

agc tgc aat ctt aag ctt aac tta gac aga cta ctt gct agg atg tgg    867
Ser Cys Asn Leu Lys Leu Asn Leu Asp Arg Leu Leu Ala Arg Met Trp
    270                 275                 280

gac gaa atg ggc ctt gtg aga gtt tac tcg aag ccg caa ggc cag caa    915
Asp Glu Met Gly Leu Val Arg Val Tyr Ser Lys Pro Gln Gly Gln Gln
285                 290                 295                 300

cca gat ttc gat gag cct ttt gtc ctc tca tct gat cga ggt ggc tgc    963
Pro Asp Phe Asp Glu Pro Phe Val Leu Ser Ser Asp Arg Gly Gly Cys
                305                 310                 315

aca gtg gaa gac ttc tgt aac cac gtc cac agg act ctg gtg aag gat    1011
Thr Val Glu Asp Phe Cys Asn His Val His Arg Thr Leu Val Lys Asp
            320                 325                 330

atg aag tat gca ctc gtt tgg ggc aca agc aca agg cac aat cca cag    1059
Met Lys Tyr Ala Leu Val Trp Gly Thr Ser Thr Arg His Asn Pro Gln
        335                 340                 345

aat tgt ggt ctt tct caa cat ctt gaa gac gaa gat gtt gtt cag atc    1107
Asn Cys Gly Leu Ser Gln His Leu Glu Asp Glu Asp Val Val Gln Ile
    350                 355                 360

gtc aag aaa aag gag aga gac gaa gga gga aga ggc cgg ttc aag tca    1155
Val Lys Lys Lys Glu Arg Asp Glu Gly Gly Arg Gly Arg Phe Lys Ser
365                 370                 375                 380
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cac tca aac gcc cct gct aga att gca gac aga gag aaa aaa gct cct     1203
His Ser Asn Ala Pro Ala Arg Ile Ala Asp Arg Glu Lys Lys Ala Pro
                385                 390                 395

ctt aag caa taa gcttttag                                             1223
Leu Lys Gln
            400


<210> 90
<211> 399
<212> PRT
<213> Arabidopsis thaliana

<400> 90
Met Gly Ile Ile Glu Arg Ile Lys Glu Ile Glu Ala Glu Met Ala Arg
 1               5                  10                  15

Thr Gln Lys Asn Lys Ala Thr Glu Tyr His Leu Gly Gln Leu Lys Ala
            20                  25                  30

Lys Ile Ala Lys Leu Arg Thr Gln Leu Leu Glu Pro Pro Lys Gly Ala
        35                  40                  45

Ser Gly Gly Gly Glu Gly Phe Glu Val Thr Lys Tyr Gly His Gly Arg
    50                  55                  60

Val Ala Leu Ile Gly Phe Pro Ser Val Gly Lys Ser Thr Leu Leu Thr
65                  70                  75                  80

Met Leu Thr Gly Thr His Ser Glu Ala Ala Ser Tyr Glu Phe Thr Thr
                85                  90                  95

Leu Thr Cys Ile Pro Gly Val Ile His Tyr Asn Asp Thr Lys Ile Gln
            100                 105                 110

Leu Leu Asp Leu Pro Gly Ile Ile Glu Gly Ala Ser Glu Gly Lys Gly
        115                 120                 125

Arg Gly Arg Gln Val Ile Ala Val Ala Lys Ser Ser Asp Leu Val Leu
    130                 135                 140

Met Val Leu Asp Ala Ser Lys Ser Glu Gly His Arg Gln Ile Leu Thr
145                 150                 155                 160

Lys Glu Leu Glu Ala Val Gly Leu Arg Leu Asn Lys Thr Pro Pro Gln
                165                 170                 175

Ile Tyr Phe Lys Lys Lys Lys Thr Gly Gly Ile Ser Phe Asn Thr Thr
            180                 185                 190

Ala Pro Leu Thr His Ile Asp Glu Lys Leu Cys Tyr Gln Ile Leu His
        195                 200                 205

Glu Tyr Lys Ile His Asn Ala Glu Val Leu Phe Arg Glu Asn Ala Thr
    210                 215                 220
```

```
Val Asp Asp Phe Ile Asp Val Ile Glu Gly Asn Arg Lys Tyr Ile Lys
225                 230                 235                 240

Cys Val Tyr Val Tyr Ile Lys Ile Asp Val Val Gly Ile Asp Asp Val
                245                 250                 255

Asp Arg Leu Ser Arg Gln Pro Asn Ser Ile Val Ile Ser Cys Asn Leu
            260                 265                 270

Lys Leu Asn Leu Asp Arg Leu Leu Ala Arg Met Trp Asp Glu Met Gly
        275                 280                 285

Leu Val Arg Val Tyr Ser Lys Pro Gln Gly Gln Gln Pro Asp Phe Asp
    290                 295                 300

Glu Pro Phe Val Leu Ser Ser Asp Arg Gly Gly Cys Thr Val Glu Asp
305                 310                 315                 320

Phe Cys Asn His Val His Arg Thr Leu Val Lys Asp Met Lys Tyr Ala
                325                 330                 335

Leu Val Trp Gly Thr Ser Thr Arg His Asn Pro Gln Asn Cys Gly Leu
            340                 345                 350

Ser Gln His Leu Glu Asp Glu Asp Val Val Gln Ile Val Lys Lys Lys
        355                 360                 365

Glu Arg Asp Glu Gly Gly Arg Gly Arg Phe Lys Ser His Ser Asn Ala
    370                 375                 380

Pro Ala Arg Ile Ala Asp Arg Glu Lys Lys Ala Pro Leu Lys Gln
385                 390                 395


<210> 91
<211> 536
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (12)..(524)

<400> 91
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             Met Thr Ser Ser Asp Gln Ser Pro Ser His Asp Val Phe
               1               5                  10

gtc tac ggc agt ttc caa gaa cca gcc gtt gtt aat tta att ctc gaa    98
Val Tyr Gly Ser Phe Gln Glu Pro Ala Val Val Asn Leu Ile Leu Glu
     15                  20                  25

tgt gct ccg gtc atg gtt tcc gct caa ctc cac ggc tat cac ttg tat    146
Cys Ala Pro Val Met Val Ser Ala Gln Leu His Gly Tyr His Leu Tyr
 30                  35                  40                  45
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aga ctt aaa ggt cgt ttg cat cca tgt att tct cct tcc gac aat gga 194
Arg Leu Lys Gly Arg Leu His Pro Cys Ile Ser Pro Ser Asp Asn Gly
50 55 60

tta atc aat ggc aag ata cta act gga tta aca gat tct cag tta gag 242
Leu Ile Asn Gly Lys Ile Leu Thr Gly Leu Thr Asp Ser Gln Leu Glu
65 70 75

agt tta gat atg att gaa gga act gaa tat gtg agg aag act gtt gaa 290
Ser Leu Asp Met Ile Glu Gly Thr Glu Tyr Val Arg Lys Thr Val Glu
80 85 90

gtt gtt ttg act gat act ttg gag aag aag caa gtt gaa aca att gta 338
Val Val Leu Thr Asp Thr Leu Glu Lys Lys Gln Val Glu Thr Ile Val
95 100 105

tgg gca aac aag gat gat cct aat atg tat gga gaa tgg gat ttc gag 386
Trp Ala Asn Lys Asp Asp Pro Asn Met Tyr Gly Glu Trp Asp Phe Glu
110 115 120 125

gaa tgg aag agg ctt cat atg gag aaa ttt ata gag gcg gcg acg aaa 434
Glu Trp Lys Arg Leu His Met Glu Lys Phe Ile Glu Ala Ala Thr Lys
130 135 140

ttc atg gag tgg aag aag aat ccg aat ggg aga agt agg gaa gag ttt 482
Phe Met Glu Trp Lys Lys Asn Pro Asn Gly Arg Ser Arg Glu Glu Phe
145 150 155

gag aag ttt gta caa gat gat tct tct ccg gct tcg gct tga 524
Glu Lys Phe Val Gln Asp Asp Ser Ser Pro Ala Ser Ala
160 165 170

agaagttgtt ta 536

<210> 92
<211> 170
<212> PRT
<213> Arabidopsis thaliana

<400> 92
Met Thr Ser Ser Asp Gln Ser Pro Ser His Asp Val Phe Val Tyr Gly
1 5 10 15

Ser Phe Gln Glu Pro Ala Val Val Asn Leu Ile Leu Glu Cys Ala Pro
20 25 30

Val Met Val Ser Ala Gln Leu His Gly Tyr His Leu Tyr Arg Leu Lys
35 40 45

Gly Arg Leu His Pro Cys Ile Ser Pro Ser Asp Asn Gly Leu Ile Asn
50 55 60

Gly Lys Ile Leu Thr Gly Leu Thr Asp Ser Gln Leu Glu Ser Leu Asp
65 70 75 80

Met Ile Glu Gly Thr Glu Tyr Val Arg Lys Thr Val Glu Val Val Leu

85 90 95

Thr Asp Thr Leu Glu Lys Lys Gln Val Glu Thr Ile Val Trp Ala Asn
100 105 110

Lys Asp Asp Pro Asn Met Tyr Gly Glu Trp Asp Phe Glu Glu Trp Lys
115 120 125

Arg Leu His Met Glu Lys Phe Ile Glu Ala Ala Thr Lys Phe Met Glu
130 135 140

Trp Lys Lys Asn Pro Asn Gly Arg Ser Arg Glu Glu Phe Glu Lys Phe
145 150 155 160

Val Gln Asp Asp Ser Ser Pro Ala Ser Ala
165 170

<210> 93
<211> 293
<212> DNA
<213> Arabidopsis thaliana

<220>
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<222> (16)..(71)

<220>
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<222> (197)..(278)

<400> 93
agagaagtaa gagaa atg gca ggt tct aac tgt gga tgt ggc tcc tcc tgc 51
Met Ala Gly Ser Asn Cys Gly Cys Gly Ser Ser Cys
1 5 10

aaa tgt ggt gat tcg tgc ag gtaaacccta gattctctct tcattaactt 101
Lys Cys Gly Asp Ser Cys Se
15

atcatgcata tatatcctaa tatacatgtg gttacatatt ccttaagata aattttgaaa 161

tcttatactt ctgttgtttt tttggtatga caaag t tgc gag aag aac tac aac 215
r Cys Glu Lys Asn Tyr Asn
20 25

aag gag tgt gat aac tgt agc tgt gga tca aac tgc agc tgc ggg tca 263
Lys Glu Cys Asp Asn Cys Ser Cys Gly Ser Asn Cys Ser Cys Gly Ser
30 35 40

agc tgt aac tgt tga agaaattatc agcat 293
Ser Cys Asn Cys
45

<210> 94

<211> 45
<212> PRT
<213> Arabidopsis thaliana

<400> 94
Met Ala Gly Ser Asn Cys Gly Cys Gly Ser Ser Cys Lys Cys Gly Asp
1 5 10 15

Ser Cys Ser Cys Glu Lys Asn Tyr Asn Lys Glu Cys Asp Asn Cys Ser
20 25 30

Cys Gly Ser Asn Cys Ser Cys Gly Ser Ser Cys Asn Cys
35 40 45

<210> 95
<211> 880
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (14)..(868)

<400> 95
cacaccaaca cca atg tct gct tct tct tta ttt aat ctc cca ttg att 49
Met Ser Ala Ser Ser Leu Phe Asn Leu Pro Leu Ile
1 5 10

cgc ctc aga tct ctc gct ctt tcg tct tct ttt tct tct ttc cga ttt 97
Arg Leu Arg Ser Leu Ala Leu Ser Ser Ser Phe Ser Ser Phe Arg Phe
15 20 25

gcc cat cgt cct ctg tca tcg att tca ccg aga aag tta ccg aat ttt 145
Ala His Arg Pro Leu Ser Ser Ile Ser Pro Arg Lys Leu Pro Asn Phe
30 35 40

cgt gct ttc tct ggt acc gct atg aca gat act aaa gat gct ggt atg 193
Arg Ala Phe Ser Gly Thr Ala Met Thr Asp Thr Lys Asp Ala Gly Met
45 50 55 60

gat gct gtt cag aga cgt ctc atg ttt gag gat gaa tgc att ctt gtt 241
Asp Ala Val Gln Arg Arg Leu Met Phe Glu Asp Glu Cys Ile Leu Val
65 70 75

gat gaa act gat cgt gtt gtg ggg cat gac agc aag tat aat tgt cat 289
Asp Glu Thr Asp Arg Val Val Gly His Asp Ser Lys Tyr Asn Cys His
80 85 90

ctg atg gaa aat att gaa gcc aag aat ttg ctg cac agg gct ttt agt 337
Leu Met Glu Asn Ile Glu Ala Lys Asn Leu Leu His Arg Ala Phe Ser
95 100 105

gta ttt tta ttc aac tcg aag tat gag ttg ctt ctc cag caa agg tca 385
Val Phe Leu Phe Asn Ser Lys Tyr Glu Leu Leu Leu Gln Gln Arg Ser
110 115 120

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aac aca aag gtt acg ttc cct cta gtg tgg act aac act tgt tgc agc    433
Asn Thr Lys Val Thr Phe Pro Leu Val Trp Thr Asn Thr Cys Cys Ser
125                 130                 135                 140

cat cct ctt tac cgt gaa tca gag ctt atc cag gac aat gca cta ggt    481
His Pro Leu Tyr Arg Glu Ser Glu Leu Ile Gln Asp Asn Ala Leu Gly
                145                 150                 155

gtg agg aat gct gca caa aga aag ctt ctc gat gag ctt ggt att gta    529
Val Arg Asn Ala Ala Gln Arg Lys Leu Leu Asp Glu Leu Gly Ile Val
            160                 165                 170

gct gaa gat gta cca gtc gat gag ttc act ccc ttg gga cgt atg ctg    577
Ala Glu Asp Val Pro Val Asp Glu Phe Thr Pro Leu Gly Arg Met Leu
        175                 180                 185

tac aag gct cct tct gat ggc aaa tgg gga gag cat gaa ctt gat tac    625
Tyr Lys Ala Pro Ser Asp Gly Lys Trp Gly Glu His Glu Leu Asp Tyr
    190                 195                 200

ttg ctc ttc atc gtg cga gac gtg aag gtt caa cca aac cca gat gaa    673
Leu Leu Phe Ile Val Arg Asp Val Lys Val Gln Pro Asn Pro Asp Glu
205                 210                 215                 220

gta gct gag atc aag tat gtg agc cgg gaa gag ctg aag gag ctg gtg    721
Val Ala Glu Ile Lys Tyr Val Ser Arg Glu Glu Leu Lys Glu Leu Val
                225                 230                 235

aag aaa gca gat gca ggt gag gaa ggt ttg aaa ctg tca cca tgg ttc    769
Lys Lys Ala Asp Ala Gly Glu Glu Gly Leu Lys Leu Ser Pro Trp Phe
            240                 245                 250

aga ttg gtg gtg gac aat ttc ttg atg aag tgg tgg gat cat gta gag    817
Arg Leu Val Val Asp Asn Phe Leu Met Lys Trp Trp Asp His Val Glu
        255                 260                 265

aaa gga act ttg gtt gaa gct ata gac atg aaa acc atc cac aaa ctc    865
Lys Gly Thr Leu Val Glu Ala Ile Asp Met Lys Thr Ile His Lys Leu
    270                 275                 280

tga acatcttttt tt                                                  880

285


<210> 96
<211> 284
<212> PRT
<213> Arabidopsis thaliana

<400> 96
Met Ser Ala Ser Ser Leu Phe Asn Leu Pro Leu Ile Arg Leu Arg Ser
  1               5                  10                  15

Leu Ala Leu Ser Ser Ser Phe Ser Ser Phe Arg Phe Ala His Arg Pro
            20                  25                  30
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Leu Ser Ser Ile Ser Pro Arg Lys Leu Pro Asn Phe Arg Ala Phe Ser
35 40 45

Gly Thr Ala Met Thr Asp Thr Lys Asp Ala Gly Met Asp Ala Val Gln
50 55 60

Arg Arg Leu Met Phe Glu Asp Glu Cys Ile Leu Val Asp Glu Thr Asp
65 70 75 80

Arg Val Val Gly His Asp Ser Lys Tyr Asn Cys His Leu Met Glu Asn
85 90 95

Ile Glu Ala Lys Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe
100 105 110

Asn Ser Lys Tyr Glu Leu Leu Leu Gln Gln Arg Ser Asn Thr Lys Val
115 120 125

Thr Phe Pro Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu Tyr
130 135 140

Arg Glu Ser Glu Leu Ile Gln Asp Asn Ala Leu Gly Val Arg Asn Ala
145 150 155 160

Ala Gln Arg Lys Leu Leu Asp Glu Leu Gly Ile Val Ala Glu Asp Val
165 170 175

Pro Val Asp Glu Phe Thr Pro Leu Gly Arg Met Leu Tyr Lys Ala Pro
180 185 190

Ser Asp Gly Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile
195 200 205

Val Arg Asp Val Lys Val Gln Pro Asn Pro Asp Glu Val Ala Glu Ile
210 215 220

Lys Tyr Val Ser Arg Glu Glu Leu Lys Glu Leu Val Lys Lys Ala Asp
225 230 235 240

Ala Gly Glu Glu Gly Leu Lys Leu Ser Pro Trp Phe Arg Leu Val Val
245 250 255

Asp Asn Phe Leu Met Lys Trp Trp Asp His Val Glu Lys Gly Thr Leu
260 265 270

Val Glu Ala Ile Asp Met Lys Thr Ile His Lys Leu
275 280

<210> 97
<211> 831
<212> DNA
<213> Arabidopsis thaliana

<220>

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<221> CDS
<222> (18)..(821)

<400> 97
tgcactactc aacctca atg gcc gcc tca aca atg gct ctc tcc tcc cct      50
                   Met Ala Ala Ser Thr Met Ala Leu Ser Ser Pro
                   1               5                   10

gcc ttc gcc ggt aag gcc gtc aag ctt tcc ccc gcg gca tca gaa gtc      98
Ala Phe Ala Gly Lys Ala Val Lys Leu Ser Pro Ala Ala Ser Glu Val
            15                  20                  25

ctt gga agc ggc cgt gtg aca atg agg aag act gtt gcc aag cca aag     146
Leu Gly Ser Gly Arg Val Thr Met Arg Lys Thr Val Ala Lys Pro Lys
        30                  35                  40

ggc cca tca ggc agc cca tgg tac gga tct gac cgt gtc aag tac ttg     194
Gly Pro Ser Gly Ser Pro Trp Tyr Gly Ser Asp Arg Val Lys Tyr Leu
    45                  50                  55

ggt cca ttc tct ggc gaa tca ccg agc tac ctt acc gga gag ttc ccc     242
Gly Pro Phe Ser Gly Glu Ser Pro Ser Tyr Leu Thr Gly Glu Phe Pro
60                  65                  70                  75

gga gac tac gga tgg gac acc gcc gga ctt tca gct gac ccc gag aca     290
Gly Asp Tyr Gly Trp Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr
                80                  85                  90

ttc gca agg aac cgt gaa cta gaa gtt atc cac agc agg tgg gct atg     338
Phe Ala Arg Asn Arg Glu Leu Glu Val Ile His Ser Arg Trp Ala Met
            95                  100                 105

ctc gga gcc cta ggc tgc gtc ttc cct gag ctt ttg gct aga aac gga     386
Leu Gly Ala Leu Gly Cys Val Phe Pro Glu Leu Leu Ala Arg Asn Gly
        110                 115                 120

gtc aag ttc gga gag gcg gtt tgg ttc aag gcc ggt tca cag atc ttc     434
Val Lys Phe Gly Glu Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe
    125                 130                 135

agc gat gga ggg ctc gat tac ttg gga aac cct agc ttg gtt cac gct     482
Ser Asp Gly Gly Leu Asp Tyr Leu Gly Asn Pro Ser Leu Val His Ala
140                 145                 150                 155

cag agc att ttg gcc att tgg gcc aca caa gtt att ttg atg gga gcc     530
Gln Ser Ile Leu Ala Ile Trp Ala Thr Gln Val Ile Leu Met Gly Ala
                160                 165                 170

gtt gaa ggc tac aga gtc gca gga aat ggg cca ttg gga gag gcc gag     578
Val Glu Gly Tyr Arg Val Ala Gly Asn Gly Pro Leu Gly Glu Ala Glu
            175                 180                 185

gac ttg ctt tac ccc ggt ggc agc ttc gac cca ttg ggt ttg gct acc     626
Asp Leu Leu Tyr Pro Gly Gly Ser Phe Asp Pro Leu Gly Leu Ala Thr
        190                 195                 200

gac cca gag gca ttc gct gag ttg aag gtg aag gag ctc aag aac gga     674
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Asp Pro Glu Ala Phe Ala Glu Leu Lys Val Lys Glu Leu Lys Asn Gly
    205                 210                 215

aga ttg gct atg ttc tct atg ttt gga ttc ttc gtt caa gcc atc gtc     722
Arg Leu Ala Met Phe Ser Met Phe Gly Phe Phe Val Gln Ala Ile Val
220                 225                 230                 235

act ggt aag gga ccg ata gag aac ctt gct gac cat ttg gcc gat cca     770
Thr Gly Lys Gly Pro Ile Glu Asn Leu Ala Asp His Leu Ala Asp Pro
                240                 245                 250

gtt aac aac aac gca tgg gcc ttc gcc acc aac ttt gtt ccc gga aag     818
Val Asn Asn Asn Ala Trp Ala Phe Ala Thr Asn Phe Val Pro Gly Lys
            255                 260                 265

tga gccaagtttt                                                      831


<210> 98
<211> 267
<212> PRT
<213> Arabidopsis thaliana

<400> 98
Met Ala Ala Ser Thr Met Ala Leu Ser Ser Pro Ala Phe Ala Gly Lys
  1               5                  10                  15

Ala Val Lys Leu Ser Pro Ala Ala Ser Glu Val Leu Gly Ser Gly Arg
            20                  25                  30

Val Thr Met Arg Lys Thr Val Ala Lys Pro Lys Gly Pro Ser Gly Ser
        35                  40                  45

Pro Trp Tyr Gly Ser Asp Arg Val Lys Tyr Leu Gly Pro Phe Ser Gly
    50                  55                  60

Glu Ser Pro Ser Tyr Leu Thr Gly Glu Phe Pro Gly Asp Tyr Gly Trp
65                  70                  75                  80

Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr Phe Ala Arg Asn Arg
                85                  90                  95

Glu Leu Glu Val Ile His Ser Arg Trp Ala Met Leu Gly Ala Leu Gly
            100                 105                 110

Cys Val Phe Pro Glu Leu Leu Ala Arg Asn Gly Val Lys Phe Gly Glu
        115                 120                 125

Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe Ser Asp Gly Gly Leu
    130                 135                 140

Asp Tyr Leu Gly Asn Pro Ser Leu Val His Ala Gln Ser Ile Leu Ala
145                 150                 155                 160

Ile Trp Ala Thr Gln Val Ile Leu Met Gly Ala Val Glu Gly Tyr Arg
                165                 170                 175
```

```
Val Ala Gly Asn Gly Pro Leu Gly Glu Ala Glu Asp Leu Leu Tyr Pro
            180                 185                 190

Gly Gly Ser Phe Asp Pro Leu Gly Leu Ala Thr Asp Pro Glu Ala Phe
        195                 200                 205

Ala Glu Leu Lys Val Lys Glu Leu Lys Asn Gly Arg Leu Ala Met Phe
    210                 215                 220

Ser Met Phe Gly Phe Phe Val Gln Ala Ile Val Thr Gly Lys Gly Pro
225                 230                 235                 240

Ile Glu Asn Leu Ala Asp His Leu Ala Asp Pro Val Asn Asn Asn Ala
                245                 250                 255

Trp Ala Phe Ala Thr Asn Phe Val Pro Gly Lys
            260                 265
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<210> 99
<211> 855
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (15)..(164)

<220>
<221> CDS
<222> (257)..(305)

<220>
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<222> (416)..(843)

<400> 99

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cacagtatta acaa atg gca gga atc aaa gtt ttc ggt cac cca gct tcc    50
                Met Ala Gly Ile Lys Val Phe Gly His Pro Ala Ser
                1               5                   10

aca gcc act aga aga gtt ctc atc gct ctt cac gag aag aat gtc gac    98
Thr Ala Thr Arg Arg Val Leu Ile Ala Leu His Glu Lys Asn Val Asp
        15                  20                  25

ttt gaa ttc gtt cat gtc gag ctc aaa gat ggt gaa cac aag aaa gag    146
Phe Glu Phe Val His Val Glu Leu Lys Asp Gly Glu His Lys Lys Glu
    30                  35                  40

cct ttc atc ctt cgc aac gtgagtacat ataacatctg tcaagccaaa           194
Pro Phe Ile Leu Arg Asn
 45                 50

atattgtatt tcatctagat actgaatctt ggtcttaaca atcttgaata atgtttttgc 254
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ag ccc ttt ggt aaa gtt cca gcc ttt gaa gat gga gac ttc aag att 301
Pro Phe Gly Lys Val Pro Ala Phe Glu Asp Gly Asp Phe Lys Ile
55 60 65

ttc g gtaaatacaa atatatatca ttatagtcat gtttacaaat ttttggtttt 355
Phe G

atgatcattg caataataga aagcagaaac actcaaaaat gtttttttt tggtgggcag 415

aa tca aga gca att act caa tac ata gct cat gaa ttc tca gac aaa 462
lu Ser Arg Ala Ile Thr Gln Tyr Ile Ala His Glu Phe Ser Asp Lys
70 75 80

gga aac aac ctt ctc tca act ggc aag gac atg gcg atc ata gcc atg 510
Gly Asn Asn Leu Leu Ser Thr Gly Lys Asp Met Ala Ile Ile Ala Met
85 90 95

ggc att gaa att gag tcg cat gag ttt gac cca gtt ggt tca aag ctt 558
Gly Ile Glu Ile Glu Ser His Glu Phe Asp Pro Val Gly Ser Lys Leu
100 105 110

gtt tgg gag caa gtc tta aag cct ttg tat ggt atg acc aca gac aaa 606
Val Trp Glu Gln Val Leu Lys Pro Leu Tyr Gly Met Thr Thr Asp Lys
115 120 125

act gtt gtt gaa gaa gaa gag gct aag cta gcc aaa gtc ctc gat gtt 654
Thr Val Val Glu Glu Glu Glu Ala Lys Leu Ala Lys Val Leu Asp Val
130 135 140 145

tac gaa cac agg ctt ggt gag tcc aag tat ttg gct tct gac cac ttc 702
Tyr Glu His Arg Leu Gly Glu Ser Lys Tyr Leu Ala Ser Asp His Phe
150 155 160

act ttg gtc gat ctt cac act atc cct gtg att caa tac tta ctt gga 750
Thr Leu Val Asp Leu His Thr Ile Pro Val Ile Gln Tyr Leu Leu Gly
165 170 175

act cca act aag aaa ctc ttc gac gag cgt cca cat gtg agt gct tgg 798
Thr Pro Thr Lys Lys Leu Phe Asp Glu Arg Pro His Val Ser Ala Trp
180 185 190

gtt gct gac atc act tca agg cct tct gct cag aag gtt ctt taa 843
Val Ala Asp Ile Thr Ser Arg Pro Ser Ala Gln Lys Val Leu
195 200 205

gtgaatctca aa 855

<210> 100
<211> 208
<212> PRT
<213> Arabidopsis thaliana

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Met Ala Gly Ile Lys Val Phe Gly His Pro Ala Ser Thr Ala Thr Arg
1 5 10 15

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Arg Val Leu Ile Ala Leu His Glu Lys Asn Val Asp Phe Glu Phe Val
            20                  25                  30

His Val Glu Leu Lys Asp Gly Glu His Lys Lys Glu Pro Phe Ile Leu
        35                  40                  45

Arg Asn Pro Phe Gly Lys Val Pro Ala Phe Glu Asp Gly Asp Phe Lys
    50                  55                  60

Ile Phe Glu Ser Arg Ala Ile Thr Gln Tyr Ile Ala His Glu Phe Ser
65                  70                  75                  80

Asp Lys Gly Asn Asn Leu Leu Ser Thr Gly Lys Asp Met Ala Ile Ile
                85                  90                  95

Ala Met Gly Ile Glu Ile Glu Ser His Glu Phe Asp Pro Val Gly Ser
            100                 105                 110

Lys Leu Val Trp Glu Gln Val Leu Lys Pro Leu Tyr Gly Met Thr Thr
        115                 120                 125

Asp Lys Thr Val Val Glu Glu Glu Glu Ala Lys Leu Ala Lys Val Leu
    130                 135                 140

Asp Val Tyr Glu His Arg Leu Gly Glu Ser Lys Tyr Leu Ala Ser Asp
145                 150                 155                 160

His Phe Thr Leu Val Asp Leu His Thr Ile Pro Val Ile Gln Tyr Leu
                165                 170                 175

Leu Gly Thr Pro Thr Lys Lys Leu Phe Asp Glu Arg Pro His Val Ser
            180                 185                 190

Ala Trp Val Ala Asp Ile Thr Ser Arg Pro Ser Ala Gln Lys Val Leu
        195                 200                 205


<210> 101
<211> 512
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (12)..(67)

<220>
<221> CDS
<222> (241)..(309)

<220>
<221> CDS
<222> (417)..(492)

<400> 101
tatctgaaaa a atg tca gag acc aac aag aat gcc ttc caa gcc ggt cag  50
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            Met Ser Glu Thr Asn Lys Asn Ala Phe Gln Ala Gly Gln
              1               5                  10

acc gct ggc aaa gct ga ggtactactc tttctctctt tgacagaact          97
Thr Ala Gly Lys Ala Gl
     15

cttaaactgg aaaaattgtt gaagctataa ctctttgaaa acagttgaaa cttgatcatt 157

actagaaatt tcagttactt gtttaattta gtttgtcgta attatgtaat tgatgatttt 217

atggttacaa tggttgtcat gta g gag aag agc aat gtt ctg ctg gac aag   268
                          u Glu Lys Ser Asn Val Leu Leu Asp Lys
                              20                  25

gcc aag gat gct gca gct ggt gct gga gct gga gca caa ca ggtaaacaat 319
Ala Lys Asp Ala Ala Ala Gly Ala Gly Ala Gly Ala Gln Gl
     30                  35                  40

ccatacacag acacataaca tataatatgt aacgaaataa acgtctttgt aagcttacat 379

gtacgcagat ttctgatatg gttatgtata tgttata g gcg gga aag agt gta    432
                                         n Ala Gly Lys Ser Val
                                                        45

tcg gat gcg gca gcg gga ggt gtt aac ttc gtg aag gac aag acc ggc   480
Ser Asp Ala Ala Ala Gly Gly Val Asn Phe Val Lys Asp Lys Thr Gly
         50                  55                  60

ctg aac aag tag agattcgggt caaatttggg                             512
Leu Asn Lys
     65


<210> 102
<211> 66
<212> PRT
<213> Arabidopsis thaliana

<400> 102
Met Ser Glu Thr Asn Lys Asn Ala Phe Gln Ala Gly Gln Thr Ala Gly
  1               5                  10                  15

Lys Ala Glu Glu Lys Ser Asn Val Leu Leu Asp Lys Ala Lys Asp Ala
             20                  25                  30

Ala Ala Gly Ala Gly Ala Gly Ala Gln Gln Ala Gly Lys Ser Val Ser
         35                  40                  45

Asp Ala Ala Ala Gly Gly Val Asn Phe Val Lys Asp Lys Thr Gly Leu
     50                  55                  60

Asn Lys
 65
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<210> 103
<211> 1138
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (11)..(1123)

<400> 103
aaaacaaaaa atg gcg act ttg gtt gat cct cct aat ggg ata agg aat 49
Met Ala Thr Leu Val Asp Pro Pro Asn Gly Ile Arg Asn
1 5 10

gaa ggg aag cat tac ttc tca atg tgg caa act ctg ttc gag atc gac 97
Glu Gly Lys His Tyr Phe Ser Met Trp Gln Thr Leu Phe Glu Ile Asp
15 20 25

act aag tac atg cct atc aag cct att ggt cgt gga gct tac ggt gtt 145
Thr Lys Tyr Met Pro Ile Lys Pro Ile Gly Arg Gly Ala Tyr Gly Val
30 35 40 45

gtc tgc tcc tct gtt aac agt gac acc aac gag aaa gtt gct atc aag 193
Val Cys Ser Ser Val Asn Ser Asp Thr Asn Glu Lys Val Ala Ile Lys
50 55 60

aag att cac aat gtt tat gag aat agg atc gat gcg ttg agg act ctt 241
Lys Ile His Asn Val Tyr Glu Asn Arg Ile Asp Ala Leu Arg Thr Leu
65 70 75

cgg gag ctc aag ctt cta cgc cat ctt cga cat gag aat gtc att gct 289
Arg Glu Leu Lys Leu Leu Arg His Leu Arg His Glu Asn Val Ile Ala
80 85 90

ttg aaa gat gtc atg atg cca att cat aag atg agc ttc aag gat gtt 337
Leu Lys Asp Val Met Met Pro Ile His Lys Met Ser Phe Lys Asp Val
95 100 105

tat ctt gtt tat gag ctc atg gac act gat ctc cac cag att atc aag 385
Tyr Leu Val Tyr Glu Leu Met Asp Thr Asp Leu His Gln Ile Ile Lys
110 115 120 125

tct tct cag cgt ctt agt aac gat cat tgc caa tac ttc ttg ttc cag 433
Ser Ser Gln Arg Leu Ser Asn Asp His Cys Gln Tyr Phe Leu Phe Gln
130 135 140

ttg ctt cga ggg ctc aag tat att cat tca gcc aat atc ctg cac cga 481
Leu Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Ile Leu His Arg
145 150 155

gat ttg aaa cct ggt aac ctt ctt gtc aac gca aac tgc gat tta aag 529
Asp Leu Lys Pro Gly Asn Leu Leu Val Asn Ala Asn Cys Asp Leu Lys
160 165 170

ata tgc gat ttt gga cta gcg cgt gcg agc aac acc aag ggt cag ttc 577
Ile Cys Asp Phe Gly Leu Ala Arg Ala Ser Asn Thr Lys Gly Gln Phe
175 180 185

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atg act gaa tat gtt gtg act cgt tgg tac cga gcc cca gag ctt ctc   625
Met Thr Glu Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu
190                 195                 200                 205

ctc tgt tgt gac aac tat gga aca tcc att gat gtt tgg tct gtt ggt   673
Leu Cys Cys Asp Asn Tyr Gly Thr Ser Ile Asp Val Trp Ser Val Gly
                210                 215                 220

tgc att ttc gcc gag ctt ctt ggt agg aaa ccg ata ttc caa gga acg   721
Cys Ile Phe Ala Glu Leu Leu Gly Arg Lys Pro Ile Phe Gln Gly Thr
            225                 230                 235

gaa tgt ctt aac cag ctt aag ctc att gtc aac att atc gga agc caa   769
Glu Cys Leu Asn Gln Leu Lys Leu Ile Val Asn Ile Ile Gly Ser Gln
        240                 245                 250

aga gaa gaa gat ctt gag ttc ata gtt aac ccg aaa gct aaa aga tac   817
Arg Glu Glu Asp Leu Glu Phe Ile Val Asn Pro Lys Ala Lys Arg Tyr
    255                 260                 265

att aga tca ctt ccg tac tca cct ggg atg tct tta tcc aga ctt tac   865
Ile Arg Ser Leu Pro Tyr Ser Pro Gly Met Ser Leu Ser Arg Leu Tyr
270                 275                 280                 285

ccg tgc gct cat gta ttg gcc atc gac ctt ctg cag aaa atg ctt gtt   913
Pro Cys Ala His Val Leu Ala Ile Asp Leu Leu Gln Lys Met Leu Val
                290                 295                 300

ttt gat ccg tca aag agg att agt gcc tct gaa gca ctc cag cat cca   961
Phe Asp Pro Ser Lys Arg Ile Ser Ala Ser Glu Ala Leu Gln His Pro
            305                 310                 315

tac atg gcg cca cta tat gac ccg aat gca aac cct cct gct caa gtt   1009
Tyr Met Ala Pro Leu Tyr Asp Pro Asn Ala Asn Pro Pro Ala Gln Val
        320                 325                 330

cct atc gat ctc gat gta gat gag gat ttg aga gag gag atg ata aga   1057
Pro Ile Asp Leu Asp Val Asp Glu Asp Leu Arg Glu Glu Met Ile Arg
    335                 340                 345

gaa atg ata tgg aat gag atg ctt cac tac cat cca caa gct tca acc   1105
Glu Met Ile Trp Asn Glu Met Leu His Tyr His Pro Gln Ala Ser Thr
350                 355                 360                 365

tta aac act gag ctc tga gctcaagtct tgttt                          1138
Leu Asn Thr Glu Leu
                370
```

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<210> 104
<211> 370
<212> PRT
<213> Arabidopsis thaliana

<400> 104
Met Ala Thr Leu Val Asp Pro Pro Asn Gly Ile Arg Asn Glu Gly Lys
```

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1               5                   10                  15

His Tyr Phe Ser Met Trp Gln Thr Leu Phe Glu Ile Asp Thr Lys Tyr
            20                  25                  30

Met Pro Ile Lys Pro Ile Gly Arg Gly Ala Tyr Gly Val Val Cys Ser
        35                  40                  45

Ser Val Asn Ser Asp Thr Asn Glu Lys Val Ala Ile Lys Lys Ile His
    50                  55                  60

Asn Val Tyr Glu Asn Arg Ile Asp Ala Leu Arg Thr Leu Arg Glu Leu
65                  70                  75                  80

Lys Leu Leu Arg His Leu Arg His Glu Asn Val Ile Ala Leu Lys Asp
                85                  90                  95

Val Met Met Pro Ile His Lys Met Ser Phe Lys Asp Val Tyr Leu Val
            100                 105                 110

Tyr Glu Leu Met Asp Thr Asp Leu His Gln Ile Ile Lys Ser Ser Gln
        115                 120                 125

Arg Leu Ser Asn Asp His Cys Gln Tyr Phe Leu Phe Gln Leu Leu Arg
    130                 135                 140

Gly Leu Lys Tyr Ile His Ser Ala Asn Ile Leu His Arg Asp Leu Lys
145                 150                 155                 160

Pro Gly Asn Leu Leu Val Asn Ala Asn Cys Asp Leu Lys Ile Cys Asp
                165                 170                 175

Phe Gly Leu Ala Arg Ala Ser Asn Thr Lys Gly Gln Phe Met Thr Glu
            180                 185                 190

Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Leu Cys Cys
        195                 200                 205

Asp Asn Tyr Gly Thr Ser Ile Asp Val Trp Ser Val Gly Cys Ile Phe
    210                 215                 220

Ala Glu Leu Leu Gly Arg Lys Pro Ile Phe Gln Gly Thr Glu Cys Leu
225                 230                 235                 240

Asn Gln Leu Lys Leu Ile Val Asn Ile Ile Gly Ser Gln Arg Glu Glu
                245                 250                 255

Asp Leu Glu Phe Ile Val Asn Pro Lys Ala Lys Arg Tyr Ile Arg Ser
            260                 265                 270

Leu Pro Tyr Ser Pro Gly Met Ser Leu Ser Arg Leu Tyr Pro Cys Ala
        275                 280                 285

His Val Leu Ala Ile Asp Leu Leu Gln Lys Met Leu Val Phe Asp Pro
    290                 295                 300

Ser Lys Arg Ile Ser Ala Ser Glu Ala Leu Gln His Pro Tyr Met Ala
```

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305                 310                 315                 320

Pro Leu Tyr Asp Pro Asn Ala Asn Pro Pro Ala Gln Val Pro Ile Asp
                325                 330                 335

Leu Asp Val Asp Glu Asp Leu Arg Glu Glu Met Ile Arg Glu Met Ile
            340                 345                 350

Trp Asn Glu Met Leu His Tyr His Pro Gln Ala Ser Thr Leu Asn Thr
        355                 360                 365

Glu Leu
    370


<210> 105
<211> 445
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (20)..(430)

<400> 105
aacaacaatt tcaagagac atg gca ggc aaa ggt gga aaa gga ctc gta gct   52
                     Met Ala Gly Lys Gly Gly Lys Gly Leu Val Ala
                       1               5                  10

gcg aag acg atg gct gct aac aag gac aaa gac aag gac aag aag aaa   100
Ala Lys Thr Met Ala Ala Asn Lys Asp Lys Asp Lys Asp Lys Lys Lys
            15                  20                  25

ccc atc tct cgc tct gct cgt gct ggt att cag ttt cca gtt gga cga   148
Pro Ile Ser Arg Ser Ala Arg Ala Gly Ile Gln Phe Pro Val Gly Arg
        30                  35                  40

att cac agg caa ctg aag acc cga gtc tcg gca cat ggc aga gtt ggt   196
Ile His Arg Gln Leu Lys Thr Arg Val Ser Ala His Gly Arg Val Gly
    45                  50                  55

gcc act gca gcc gtc tac aca gct tca atc ctg gag tat ctg aca gca   244
Ala Thr Ala Ala Val Tyr Thr Ala Ser Ile Leu Glu Tyr Leu Thr Ala
60                  65                  70                  75

gag gtt ctt gag ttg gct ggg aat gcg agc aag gat ctc aaa gtg aag   292
Glu Val Leu Glu Leu Ala Gly Asn Ala Ser Lys Asp Leu Lys Val Lys
                80                  85                  90

agg ata acg cca agg cat ctg cag ttg gcg att aga gga gat gag gag   340
Arg Ile Thr Pro Arg His Leu Gln Leu Ala Ile Arg Gly Asp Glu Glu
            95                  100                 105

ctg gac aca ctc atc aag gga acg att gct gga ggt ggt gtg atc cct   388
Leu Asp Thr Leu Ile Lys Gly Thr Ile Ala Gly Gly Gly Val Ile Pro
        110                 115                 120
```

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cac atc cac aag tct ctc atc aac aaa acc acc aag gag tga            430
His Ile His Lys Ser Leu Ile Asn Lys Thr Thr Lys Glu
    125                 130                 135

tgtgtagctt tttat                                                   445


&lt;210&gt; 106
&lt;211&gt; 136
&lt;212&gt; PRT
&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 106
Met Ala Gly Lys Gly Gly Lys Gly Leu Val Ala Ala Lys Thr Met Ala
 1               5                  10                  15

Ala Asn Lys Asp Lys Asp Lys Asp Lys Lys Lys Pro Ile Ser Arg Ser
            20                  25                  30

Ala Arg Ala Gly Ile Gln Phe Pro Val Gly Arg Ile His Arg Gln Leu
        35                  40                  45

Lys Thr Arg Val Ser Ala His Gly Arg Val Gly Ala Thr Ala Ala Val
    50                  55                  60

Tyr Thr Ala Ser Ile Leu Glu Tyr Leu Thr Ala Glu Val Leu Glu Leu
65                  70                  75                  80

Ala Gly Asn Ala Ser Lys Asp Leu Lys Val Lys Arg Ile Thr Pro Arg
                85                  90                  95

His Leu Gln Leu Ala Ile Arg Gly Asp Glu Glu Leu Asp Thr Leu Ile
            100                 105                 110

Lys Gly Thr Ile Ala Gly Gly Gly Val Ile Pro His Ile His Lys Ser
        115                 120                 125

Leu Ile Asn Lys Thr Thr Lys Glu
    130                 135


&lt;210&gt; 107
&lt;211&gt; 930
&lt;212&gt; DNA
&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; (14)..(916)

&lt;400&gt; 107
gcctccttgg ctt atg tac tta cca aaa cgt ggc aat ttg ttc gaa ctc      49
               Met Tyr Leu Pro Lys Arg Gly Asn Leu Phe Glu Leu
                1               5                  10
```

tat gat cca ttg cat cag aag atg tac aca ttg aat cta cct gag ctt 97
Tyr Asp Pro Leu His Gln Lys Met Tyr Thr Leu Asn Leu Pro Glu Leu
15 20 25

gcc aaa tct acg gtt tgt tac tca aga gat gga tgg tta cta atg cgt 145
Ala Lys Ser Thr Val Cys Tyr Ser Arg Asp Gly Trp Leu Leu Met Arg
30 35 40

aaa acc att tca aga gaa atg ttc ttc ttc aac ccg ttt act cgt gag 193
Lys Thr Ile Ser Arg Glu Met Phe Phe Phe Asn Pro Phe Thr Arg Glu
45 50 55 60

ctc ata aac gta cca aaa tgt act tta tca tat gat gcg atc gct ttc 241
Leu Ile Asn Val Pro Lys Cys Thr Leu Ser Tyr Asp Ala Ile Ala Phe
65 70 75

tct tgt gca cct aca tca ggt act tgc gtg ttg cta gca ttt aag cat 289
Ser Cys Ala Pro Thr Ser Gly Thr Cys Val Leu Leu Ala Phe Lys His
80 85 90

gtt tcg tat cgt atc acc act acg agc act tgc cat ccc aaa gca acc 337
Val Ser Tyr Arg Ile Thr Thr Thr Ser Thr Cys His Pro Lys Ala Thr
95 100 105

gag tgg gtt act gag gat cta caa ttc cat cgt cgc ttc cgc agt gaa 385
Glu Trp Val Thr Glu Asp Leu Gln Phe His Arg Arg Phe Arg Ser Glu
110 115 120

aca ctt aac cac agc aat gtt gtc tat gcc aaa cgt cgc ttc tat tgc 433
Thr Leu Asn His Ser Asn Val Val Tyr Ala Lys Arg Arg Phe Tyr Cys
125 130 135 140

ctt gac ggt caa gga agc tta tat tac ttt gat ccg tct tct cga aga 481
Leu Asp Gly Gln Gly Ser Leu Tyr Tyr Phe Asp Pro Ser Ser Arg Arg
145 150 155

tgg gat ttt agt tac acc tat tta ctg cca tgt cct tat atc tcg gat 529
Trp Asp Phe Ser Tyr Thr Tyr Leu Leu Pro Cys Pro Tyr Ile Ser Asp
160 165 170

aga ttt agt tac cag tat gag cgg aag aag aag aga att ttc ttg gct 577
Arg Phe Ser Tyr Gln Tyr Glu Arg Lys Lys Lys Arg Ile Phe Leu Ala
175 180 185

gtg cgg aaa gga gtg ttc ttt aag ata ttt aca tgt gat ggt gag aag 625
Val Arg Lys Gly Val Phe Phe Lys Ile Phe Thr Cys Asp Gly Glu Lys
190 195 200

ccg ata gtg cat aag tta gaa gat atc aat tgg gag gag atc aat agt 673
Pro Ile Val His Lys Leu Glu Asp Ile Asn Trp Glu Glu Ile Asn Ser
205 210 215 220

act acg att gat gga ttg aca atc ttt acg ggt ctt tat tcc tct gag 721
Thr Thr Ile Asp Gly Leu Thr Ile Phe Thr Gly Leu Tyr Ser Ser Glu
225 230 235

gtg aga ctt aat cta cca tgg atg agg aat agt gtt tac ttt cct aga 769

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Val Arg Leu Asn Leu Pro Trp Met Arg Asn Ser Val Tyr Phe Pro Arg
            240                 245                 250

ctt cgt ttt aat gtc aag cgt tgt gta tca tat tcg ctt gat gaa gag     817
Leu Arg Phe Asn Val Lys Arg Cys Val Ser Tyr Ser Leu Asp Glu Glu
        255                 260                 265

agg tat tat ccg cgg aag cag tgg caa gaa cag gag gat tta tgt cct     865
Arg Tyr Tyr Pro Arg Lys Gln Trp Gln Glu Gln Glu Asp Leu Cys Pro
    270                 275                 280

att gag aat ctt tgg att agg cca ccg aag aaa gct gta gat ttc atg     913
Ile Glu Asn Leu Trp Ile Arg Pro Pro Lys Lys Ala Val Asp Phe Met
285                 290                 295                 300

tga agataaaagt aatg                                                 930


<210> 108
<211> 300
<212> PRT
<213> Arabidopsis thaliana

<400> 108
Met Tyr Leu Pro Lys Arg Gly Asn Leu Phe Glu Leu Tyr Asp Pro Leu
  1               5                  10                  15

His Gln Lys Met Tyr Thr Leu Asn Leu Pro Glu Leu Ala Lys Ser Thr
             20                  25                  30

Val Cys Tyr Ser Arg Asp Gly Trp Leu Leu Met Arg Lys Thr Ile Ser
         35                  40                  45

Arg Glu Met Phe Phe Phe Asn Pro Phe Thr Arg Glu Leu Ile Asn Val
     50                  55                  60

Pro Lys Cys Thr Leu Ser Tyr Asp Ala Ile Ala Phe Ser Cys Ala Pro
 65                  70                  75                  80

Thr Ser Gly Thr Cys Val Leu Leu Ala Phe Lys His Val Ser Tyr Arg
                 85                  90                  95

Ile Thr Thr Thr Ser Thr Cys His Pro Lys Ala Thr Glu Trp Val Thr
            100                 105                 110

Glu Asp Leu Gln Phe His Arg Arg Phe Arg Ser Glu Thr Leu Asn His
        115                 120                 125

Ser Asn Val Val Tyr Ala Lys Arg Arg Phe Tyr Cys Leu Asp Gly Gln
    130                 135                 140

Gly Ser Leu Tyr Tyr Phe Asp Pro Ser Ser Arg Arg Trp Asp Phe Ser
145                 150                 155                 160

Tyr Thr Tyr Leu Leu Pro Cys Pro Tyr Ile Ser Asp Arg Phe Ser Tyr
                165                 170                 175
```

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Gln Tyr Glu Arg Lys Lys Lys Arg Ile Phe Leu Ala Val Arg Lys Gly
            180                 185                 190

Val Phe Phe Lys Ile Phe Thr Cys Asp Gly Glu Lys Pro Ile Val His
        195                 200                 205

Lys Leu Glu Asp Ile Asn Trp Glu Glu Ile Asn Ser Thr Thr Ile Asp
    210                 215                 220

Gly Leu Thr Ile Phe Thr Gly Leu Tyr Ser Ser Glu Val Arg Leu Asn
225                 230                 235                 240

Leu Pro Trp Met Arg Asn Ser Val Tyr Phe Pro Arg Leu Arg Phe Asn
                245                 250                 255

Val Lys Arg Cys Val Ser Tyr Ser Leu Asp Glu Glu Arg Tyr Tyr Pro
            260                 265                 270

Arg Lys Gln Trp Gln Glu Gln Glu Asp Leu Cys Pro Ile Glu Asn Leu
        275                 280                 285

Trp Ile Arg Pro Pro Lys Lys Ala Val Asp Phe Met
    290                 295                 300


<210> 109
<211> 2640
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (145)..(981)

<220>
<221> CDS
<222> (1439)..(1727)

<220>
<221> CDS
<222> (1817)..(2126)

<220>
<221> CDS
<222> (2204)..(2330)

<220>
<221> CDS
<222> (2405)..(2518)

<400> 109
tccacggcta caaaagaaca ttctcgacat acacaaaaaa attcgaaatt tcgagaactc 60

tcttgtgcct tcttcttcat cttcctctgt ttttaaaaat gcaatcaagc agattctcac 120
```

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gatacctaaa ccaaatccaa ttca atg gcg gaa gaa gca aaa tcc aaa gga    171
                           Met Ala Glu Glu Ala Lys Ser Lys Gly
                            1               5

aac gca gct ttc tct tcc ggc gat tac gcc acc gca ata acc cat ttc   219
Asn Ala Ala Phe Ser Ser Gly Asp Tyr Ala Thr Ala Ile Thr His Phe
 10                  15                  20                  25

aca gaa gca atc aac ctt tca cca acc aat cac atc ctc tac tca aac   267
Thr Glu Ala Ile Asn Leu Ser Pro Thr Asn His Ile Leu Tyr Ser Asn
                 30                  35                  40

aga tcc gct tct tac gct tct ctc cac cgt tac gaa gaa gct tta tca   315
Arg Ser Ala Ser Tyr Ala Ser Leu His Arg Tyr Glu Glu Ala Leu Ser
             45                  50                  55

gac gcg aag aag act ata gag ctt aaa cct gat tgg tct aaa gga tat   363
Asp Ala Lys Lys Thr Ile Glu Leu Lys Pro Asp Trp Ser Lys Gly Tyr
         60                  65                  70

agc cga tta ggt gct gcg ttt att gga ttg tcc aag ttt gat gaa gcg   411
Ser Arg Leu Gly Ala Ala Phe Ile Gly Leu Ser Lys Phe Asp Glu Ala
     75                  80                  85

gtt gat tcg tat aag aaa gga tta gag att gat ccg agt aat gag atg   459
Val Asp Ser Tyr Lys Lys Gly Leu Glu Ile Asp Pro Ser Asn Glu Met
 90                  95                 100                 105

ctt aaa tcg gga tta gct gat gct tcg aga tct agg gtt tcg tca aag   507
Leu Lys Ser Gly Leu Ala Asp Ala Ser Arg Ser Arg Val Ser Ser Lys
                110                 115                 120

tcg aat cct ttt gtt gat gcg ttt caa ggg aag gag atg tgg gag aag   555
Ser Asn Pro Phe Val Asp Ala Phe Gln Gly Lys Glu Met Trp Glu Lys
            125                 130                 135

ttg acg gcg gat ccg ggg act agg gtt tat ttg gag cag gat gat ttt   603
Leu Thr Ala Asp Pro Gly Thr Arg Val Tyr Leu Glu Gln Asp Asp Phe
        140                 145                 150

gtt aag acg atg aag gag att cag agg aac cct aat aat ctt aat ttg   651
Val Lys Thr Met Lys Glu Ile Gln Arg Asn Pro Asn Asn Leu Asn Leu
    155                 160                 165

tat atg aag gat aag aga gtt atg aag gct tta ggg gtt ttg ttg aat   699
Tyr Met Lys Asp Lys Arg Val Met Lys Ala Leu Gly Val Leu Leu Asn
170                 175                 180                 185

gtg aag ttt ggt gga tct agt ggt gaa gat act gag atg aag gag gct   747
Val Lys Phe Gly Gly Ser Ser Gly Glu Asp Thr Glu Met Lys Glu Ala
                190                 195                 200

gat gag agg aaa gag cct gaa ccg gag atg gaa cct atg gag ttg acg   795
Asp Glu Arg Lys Glu Pro Glu Pro Glu Met Glu Pro Met Glu Leu Thr
            205                 210                 215

gag gag gag agg cag aag aag gag aga aag gag aag gct ttg aag gag   843
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Glu Glu Glu Arg Gln Lys Lys Glu Arg Lys Glu Lys Ala Leu Lys Glu
        220                 225                 230

aaa ggg gaa gga aat gtt gct tat aag aag aag gat ttt ggg aga gct    891
Lys Gly Glu Gly Asn Val Ala Tyr Lys Lys Lys Asp Phe Gly Arg Ala
    235                 240                 245

gtt gaa cat tat act aag gcc atg gag ctc gat gat gag gat att tcg    939
Val Glu His Tyr Thr Lys Ala Met Glu Leu Asp Asp Glu Asp Ile Ser
250                 255                 260                 265

tat ttg acg aat cgt gct gct gtt tat ctt gag atg ggg aag            981
Tyr Leu Thr Asn Arg Ala Ala Val Tyr Leu Glu Met Gly Lys
                270                 275

gtattaagtc ttatacttgg cttaaaagtt aaacctttag gtactttaag attaaggagg 1041

agatcttggg ttcttgaagt agcttatctg tttagtatag cttgtcacta gttagtacat 1101

ttgtgatgac cttgatgggt tttgataact ttcatctgct tcttgttgga gatttaagag 1161

ttttgaactt aagttttcac ttgtgctgaa agtagttagc tttagatgag gtagaaattt 1221

agggtttatg gcttcatgat ggagtttatt cacttgttct gtagaagtgg ttatctttat 1281

tattactgga atcaattaat cttcaagtat cctgagtggt tcaattccat tggtctatgt 1341

gttcttgcat tagtcttgtt taattaacag ttggttcatc tggatcttac tgtatcttgt 1401

gtgatgtttt acttcatttc tcaaatgaaa ttatcag tac gag gag tgc att gaa  1456
                                         Tyr Glu Glu Cys Ile Glu
                                         280                 285

gac tgt gac aag gct gtt gaa aga ggc aga gaa ctt cgt tct gac ttc   1504
Asp Cys Asp Lys Ala Val Glu Arg Gly Arg Glu Leu Arg Ser Asp Phe
                290                 295                 300

aag atg ata gca aga gct ctg act aga aaa gga tct gct cta gtg aaa   1552
Lys Met Ile Ala Arg Ala Leu Thr Arg Lys Gly Ser Ala Leu Val Lys
            305                 310                 315

atg gcg aga tgc tcg aaa gac ttt gag cct gcg att gag act ttc cag   1600
Met Ala Arg Cys Ser Lys Asp Phe Glu Pro Ala Ile Glu Thr Phe Gln
        320                 325                 330

aaa gct ctt aca gag cat cgt aat cca gat aca ttg aag aaa ctg aac   1648
Lys Ala Leu Thr Glu His Arg Asn Pro Asp Thr Leu Lys Lys Leu Asn
    335                 340                 345

gat gct gag aaa gtc aag aaa gag ctg gag caa cag gag tac ttt gat   1696
Asp Ala Glu Lys Val Lys Lys Glu Leu Glu Gln Gln Glu Tyr Phe Asp
350                 355                 360                 365

cct acg ata gcc gag gag gag cga gag aaa g gtatatatac tgatcctcag   1747
Pro Thr Ile Ala Glu Glu Glu Arg Glu Lys G
                370                 375
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ttacacttac tatcttgaaa cgtgatttga ttttaggatt aagcatttga cacttcttca 1807

ttgatgcag gt aat gga ttc ttt aaa gaa caa aag tat cca gag gca gtg   1857
          ly Asn Gly Phe Phe Lys Glu Gln Lys Tyr Pro Glu Ala Val
                         380                 385

aag cat tat tca gaa gca atc aaa aga aac ccg aac gac gtg agg gca   1905
Lys His Tyr Ser Glu Ala Ile Lys Arg Asn Pro Asn Asp Val Arg Ala
390                 395                 400                 405

tat agc aac aga gct gct tgt tac aca aag tta gga gca tta cca gag   1953
Tyr Ser Asn Arg Ala Ala Cys Tyr Thr Lys Leu Gly Ala Leu Pro Glu
                410                 415                 420

gga ttg aaa gat gct gaa aaa tgc att gag ctg gac cca agt ttc acg   2001
Gly Leu Lys Asp Ala Glu Lys Cys Ile Glu Leu Asp Pro Ser Phe Thr
            425                 430                 435

aaa gga tac agt aga aaa gga gct att caa ttt ttc atg aag gaa tac   2049
Lys Gly Tyr Ser Arg Lys Gly Ala Ile Gln Phe Phe Met Lys Glu Tyr
        440                 445                 450

gat aaa gct atg gaa acg tat caa gaa ggg cta aaa cat gat cct aag   2097
Asp Lys Ala Met Glu Thr Tyr Gln Glu Gly Leu Lys His Asp Pro Lys
    455                 460                 465

aac cag gag ttc ctt gat ggt gtt aga ag gtttgcaaat tttggcattc      2146
Asn Gln Glu Phe Leu Asp Gly Val Arg Ar
470                 475

tctctttgtt gtttaacctt gcaaagatcg gtctagtgaa agtgttgttg ttttcag a  2204
                                                              g

tgt gtg gaa cag ata aac aaa gcg agc cgt ggt gat ctg act cca gaa   2252
Cys Val Glu Gln Ile Asn Lys Ala Ser Arg Gly Asp Leu Thr Pro Glu
480                 485                 490                 495

gaa ttg aag gag aga caa gca aag gca atg caa gat cct gaa gtt cag   2300
Glu Leu Lys Glu Arg Gln Ala Lys Ala Met Gln Asp Pro Glu Val Gln
                500                 505                 510

aac ata tta tcg gat cca gtg atg aga cag gtaaaagcag tggcaagcat     2350
Asn Ile Leu Ser Asp Pro Val Met Arg Gln
            515                 520

tgtgttctaa ctcgtaagct gtctgtgaga cttgtgtgat gatgtctatt gtag gta   2407
                                                            Val

cta gtg gac ttt caa gag aat ccg aaa gct gca caa gag cat atg aag   2455
Leu Val Asp Phe Gln Glu Asn Pro Lys Ala Ala Gln Glu His Met Lys
        525                 530                 535

aac cca atg gta atg aac aag att cag aag ctg gtt agt gcc gga att   2503
Asn Pro Met Val Met Asn Lys Ile Gln Lys Leu Val Ser Ala Gly Ile
    540                 545                 550

gtt cag gtc cgg taa attggttatg ctaaaccgga gtggtatatt gaatcaaacc   2558
```

Val Gln Val Arg
555

gaagatgttt ccaaattttc actgcgttct tttgggcttt tgttaaactg atgaaactct 2618

gatttggttt gggtcatgtt tg 2640

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1 5 10 15

Asp Tyr Ala Thr Ala Ile Thr His Phe Thr Glu Ala Ile Asn Leu Ser
20 25 30

Pro Thr Asn His Ile Leu Tyr Ser Asn Arg Ser Ala Ser Tyr Ala Ser
35 40 45

Leu His Arg Tyr Glu Glu Ala Leu Ser Asp Ala Lys Lys Thr Ile Glu
50 55 60

Leu Lys Pro Asp Trp Ser Lys Gly Tyr Ser Arg Leu Gly Ala Ala Phe
65 70 75 80

Ile Gly Leu Ser Lys Phe Asp Glu Ala Val Asp Ser Tyr Lys Lys Gly
85 90 95

Leu Glu Ile Asp Pro Ser Asn Glu Met Leu Lys Ser Gly Leu Ala Asp
100 105 110

Ala Ser Arg Ser Arg Val Ser Ser Lys Ser Asn Pro Phe Val Asp Ala
115 120 125

Phe Gln Gly Lys Glu Met Trp Glu Lys Leu Thr Ala Asp Pro Gly Thr
130 135 140

Arg Val Tyr Leu Glu Gln Asp Asp Phe Val Lys Thr Met Lys Glu Ile
145 150 155 160

Gln Arg Asn Pro Asn Asn Leu Asn Leu Tyr Met Lys Asp Lys Arg Val
165 170 175

Met Lys Ala Leu Gly Val Leu Leu Asn Val Lys Phe Gly Gly Ser Ser
180 185 190

Gly Glu Asp Thr Glu Met Lys Glu Ala Asp Glu Arg Lys Glu Pro Glu
195 200 205

Pro Glu Met Glu Pro Met Glu Leu Thr Glu Glu Glu Arg Gln Lys Lys
210 215 220

Glu Arg Lys Glu Lys Ala Leu Lys Glu Lys Gly Glu Gly Asn Val Ala

225 230 235 240

Tyr Lys Lys Lys Asp Phe Gly Arg Ala Val Glu His Tyr Thr Lys Ala
245 250 255

Met Glu Leu Asp Asp Glu Asp Ile Ser Tyr Leu Thr Asn Arg Ala Ala
260 265 270

Val Tyr Leu Glu Met Gly Lys Tyr Glu Glu Cys Ile Glu Asp Cys Asp
275 280 285

Lys Ala Val Glu Arg Gly Arg Glu Leu Arg Ser Asp Phe Lys Met Ile
290 295 300

Ala Arg Ala Leu Thr Arg Lys Gly Ser Ala Leu Val Lys Met Ala Arg
305 310 315 320

Cys Ser Lys Asp Phe Glu Pro Ala Ile Glu Thr Phe Gln Lys Ala Leu
325 330 335

Thr Glu His Arg Asn Pro Asp Thr Leu Lys Lys Leu Asn Asp Ala Glu
340 345 350

Lys Val Lys Lys Glu Leu Glu Gln Gln Glu Tyr Phe Asp Pro Thr Ile
355 360 365

Ala Glu Glu Glu Arg Glu Lys Gly Asn Gly Phe Phe Lys Glu Gln Lys
370 375 380

Tyr Pro Glu Ala Val Lys His Tyr Ser Glu Ala Ile Lys Arg Asn Pro
385 390 395 400

Asn Asp Val Arg Ala Tyr Ser Asn Arg Ala Ala Cys Tyr Thr Lys Leu
405 410 415

Gly Ala Leu Pro Glu Gly Leu Lys Asp Ala Glu Lys Cys Ile Glu Leu
420 425 430

Asp Pro Ser Phe Thr Lys Gly Tyr Ser Arg Lys Gly Ala Ile Gln Phe
435 440 445

Phe Met Lys Glu Tyr Asp Lys Ala Met Glu Thr Tyr Gln Glu Gly Leu
450 455 460

Lys His Asp Pro Lys Asn Gln Glu Phe Leu Asp Gly Val Arg Arg Cys
465 470 475 480

Val Glu Gln Ile Asn Lys Ala Ser Arg Gly Asp Leu Thr Pro Glu Glu
485 490 495

Leu Lys Glu Arg Gln Ala Lys Ala Met Gln Asp Pro Glu Val Gln Asn
500 505 510

Ile Leu Ser Asp Pro Val Met Arg Gln Val Leu Val Asp Phe Gln Glu
515 520 525

Asn Pro Lys Ala Ala Gln Glu His Met Lys Asn Pro Met Val Met Asn

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    530                 535                 540

Lys Ile Gln Lys Leu Val Ser Ala Gly Ile Val Gln Val Arg
545                 550                 555



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ataagagaga gagaagaaaa aaagaattac aattaataag aacaagatca agaatcaaga 120

atcaagaaa atg gga aga gca ccg tgt tgt gat aag gcc aac gtg aag aaa 171
          Met Gly Arg Ala Pro Cys Cys Asp Lys Ala Asn Val Lys Lys
            1               5                   10

ggg cct tgg tct cct gag gaa gac gcc aaa ctc aaa gat tac atc gag   219
Gly Pro Trp Ser Pro Glu Glu Asp Ala Lys Leu Lys Asp Tyr Ile Glu
 15                 20                  25                  30

aat agt ggc aca gga ggc aac tgg att gct ttg cct cag aaa att g     265
Asn Ser Gly Thr Gly Gly Asn Trp Ile Ala Leu Pro Gln Lys Ile G
                35                  40                  45

gtatgtatta cttaaaactc acttttgatt taaaattggc actgagagtt tccaaatagt 325

actttgagac cgtggtcgtg ttaaatttgt gtgttgatga tatttattta catggtatag 385

gt tta agg aga tgt ggg aag agt tgc agg cta agg tgg ctc aac tat    432
ly Leu Arg Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr
               50                  55                  60

ttg aga cca aac atc aaa cat ggt ggc ttc tcc gag gaa gaa gac aac   480
Leu Arg Pro Asn Ile Lys His Gly Gly Phe Ser Glu Glu Glu Asp Asn
            65                  70                  75

atc att tgt aac ctc tat gtt act att ggt agc ag gtactatata         525
Ile Ile Cys Asn Leu Tyr Val Thr Ile Gly Ser Ar
        80                  85
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cttacatata tatcatcata tgcatggatg aatattatta attgacacac ttattcttga 585

cttagagact cactatgtat ctttgtttaa ttctag g tgg tct ata att gct gca 640
g Trp Ser Ile Ile Ala Ala
90 95

caa ttg ccg gga aga acc gac aac gat atc aaa aac tat tgg aac acg 688
Gln Leu Pro Gly Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr
100 105 110

agg ctg aag aag aag ctt ctg aac aaa caa agg aaa gag ttc caa gaa 736
Arg Leu Lys Lys Lys Leu Leu Asn Lys Gln Arg Lys Glu Phe Gln Glu
115 120 125

gcg cga atg aag caa gag atg gtg atg atg aaa agg caa caa caa gga 784
Ala Arg Met Lys Gln Glu Met Val Met Met Lys Arg Gln Gln Gln Gly
130 135 140

caa gga caa ggt caa agt aat ggt agt acg gat ctt tat ctt aac aac 832
Gln Gly Gln Gly Gln Ser Asn Gly Ser Thr Asp Leu Tyr Leu Asn Asn
145 150 155

atg ttt gga tca tca cca tgg cca tta cta cca caa ctt cct cct cca 880
Met Phe Gly Ser Ser Pro Trp Pro Leu Leu Pro Gln Leu Pro Pro Pro
160 165 170 175

cat cat caa ata cct ctt gga atg atg gaa cca aca agc tgt aac tac 928
His His Gln Ile Pro Leu Gly Met Met Glu Pro Thr Ser Cys Asn Tyr
180 185 190

tac caa acg aca ccg tct tgt aac cta gaa caa aag cca ttg atc aca 976
Tyr Gln Thr Thr Pro Ser Cys Asn Leu Glu Gln Lys Pro Leu Ile Thr
195 200 205

ctc aag aac atg gtc aag att gaa gaa gaa cag gaa agg aca aac cct 1024
Leu Lys Asn Met Val Lys Ile Glu Glu Glu Gln Glu Arg Thr Asn Pro
210 215 220

gat cat cat cat caa gat tct gtc aca aac cct ttt gat ttc tct ttc 1072
Asp His His His Gln Asp Ser Val Thr Asn Pro Phe Asp Phe Ser Phe
225 230 235

tct cag ctt ttg tta gat ccc aat tac tat ctg gga tca gga ggg gga 1120
Ser Gln Leu Leu Leu Asp Pro Asn Tyr Tyr Leu Gly Ser Gly Gly Gly
240 245 250 255

gga gaa gga gat ttt gct atc atg agc agc agc aca aac tca cca tta 1168
Gly Glu Gly Asp Phe Ala Ile Met Ser Ser Ser Thr Asn Ser Pro Leu
260 265 270

cca aac aca agt agt gat caa cat cca agt caa cag caa gag att ctt 1216
Pro Asn Thr Ser Ser Asp Gln His Pro Ser Gln Gln Gln Glu Ile Leu
275 280 285

caa tgg ttt ggg agc agt aac ttt cag aca gaa gca atc aac gat atg 1264
Gln Trp Phe Gly Ser Ser Asn Phe Gln Thr Glu Ala Ile Asn Asp Met
290 295 300

ttc ata aac aac aac aac aac ata gtg aat ctt gag acc atc gag aac 1312
Phe Ile Asn Asn Asn Asn Asn Ile Val Asn Leu Glu Thr Ile Glu Asn
305 310 315

aca aaa gtc tat gga gac gcc tca gta gcc gga gcc gct gtc cga gca 1360
Thr Lys Val Tyr Gly Asp Ala Ser Val Ala Gly Ala Ala Val Arg Ala
320 325 330 335

gct ttg ggc gga ggg aca acg agt aca tcg gcg gat caa agt aca ata 1408
Ala Leu Gly Gly Gly Thr Thr Ser Thr Ser Ala Asp Gln Ser Thr Ile
340 345 350

agt tgg gag gat ata act tct cta gtt aat tcc gaa gat gca agt tac 1456
Ser Trp Glu Asp Ile Thr Ser Leu Val Asn Ser Glu Asp Ala Ser Tyr
355 360 365

ttc aat gcg cca aat cat gtg taa cattttgttt aaaactttat ttgtacttaa 1510
Phe Asn Ala Pro Asn His Val
370 375

atacataaag aggggttttc tattttgtat aaatctgtgt ctttagggag 1560

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Trp Ser Pro Glu Glu Asp Ala Lys Leu Lys Asp Tyr Ile Glu Asn Ser
20 25 30

Gly Thr Gly Gly Asn Trp Ile Ala Leu Pro Gln Lys Ile Gly Leu Arg
35 40 45

Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro
50 55 60

Asn Ile Lys His Gly Gly Phe Ser Glu Glu Glu Asp Asn Ile Ile Cys
65 70 75 80

Asn Leu Tyr Val Thr Ile Gly Ser Arg Trp Ser Ile Ile Ala Ala Gln
85 90 95

Leu Pro Gly Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr Arg
100 105 110

Leu Lys Lys Lys Leu Leu Asn Lys Gln Arg Lys Glu Phe Gln Glu Ala
115 120 125

Arg Met Lys Gln Glu Met Val Met Met Lys Arg Gln Gln Gln Gly Gln
130 135 140

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Gly Gln Gly Gln Ser Asn Gly Ser Thr Asp Leu Tyr Leu Asn Asn Met
145                 150                 155                 160

Phe Gly Ser Ser Pro Trp Pro Leu Leu Pro Gln Leu Pro Pro Pro His
                165                 170                 175

His Gln Ile Pro Leu Gly Met Met Glu Pro Thr Ser Cys Asn Tyr Tyr
            180                 185                 190

Gln Thr Thr Pro Ser Cys Asn Leu Glu Gln Lys Pro Leu Ile Thr Leu
        195                 200                 205

Lys Asn Met Val Lys Ile Glu Glu Glu Gln Glu Arg Thr Asn Pro Asp
    210                 215                 220

His His His Gln Asp Ser Val Thr Asn Pro Phe Asp Phe Ser Phe Ser
225                 230                 235                 240

Gln Leu Leu Leu Asp Pro Asn Tyr Tyr Leu Gly Ser Gly Gly Gly Gly
                245                 250                 255

Glu Gly Asp Phe Ala Ile Met Ser Ser Ser Thr Asn Ser Pro Leu Pro
            260                 265                 270

Asn Thr Ser Ser Asp Gln His Pro Ser Gln Gln Gln Glu Ile Leu Gln
        275                 280                 285

Trp Phe Gly Ser Ser Asn Phe Gln Thr Glu Ala Ile Asn Asp Met Phe
    290                 295                 300

Ile Asn Asn Asn Asn Asn Ile Val Asn Leu Glu Thr Ile Glu Asn Thr
305                 310                 315                 320

Lys Val Tyr Gly Asp Ala Ser Val Ala Gly Ala Ala Val Arg Ala Ala
                325                 330                 335

Leu Gly Gly Gly Thr Thr Ser Thr Ser Ala Asp Gln Ser Thr Ile Ser
            340                 345                 350

Trp Glu Asp Ile Thr Ser Leu Val Asn Ser Glu Asp Ala Ser Tyr Phe
        355                 360                 365

Asn Ala Pro Asn His Val
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                                         Met Val Trp Phe Arg Ile
                                         1               5

ggt tct tct gtg gca aag ctt gcc ata aga agg aca ctg tct cag tct   103
Gly Ser Ser Val Ala Lys Leu Ala Ile Arg Arg Thr Leu Ser Gln Ser
            10                  15                  20

cgt tgt ggt tca tat gcc act aga aca agg gtt ttg cct tgt caa acc   151
Arg Cys Gly Ser Tyr Ala Thr Arg Thr Arg Val Leu Pro Cys Gln Thr
        25                  30                  35

aga tgt ttt cac tct aca ata ctc aaa tca aag gca gag tct gct gca   199
Arg Cys Phe His Ser Thr Ile Leu Lys Ser Lys Ala Glu Ser Ala Ala
    40                  45                  50

cct gtt cca cgt cct gtc cca ctt tct aag cta act gat agc ttc tta   247
Pro Val Pro Arg Pro Val Pro Leu Ser Lys Leu Thr Asp Ser Phe Leu
55                  60                  65                  70

gat gga aca agc agt gtg tat cta gag gag tta caa aga gct tgg gag   295
Asp Gly Thr Ser Ser Val Tyr Leu Glu Glu Leu Gln Arg Ala Trp Glu
                75                  80                  85

gct gat ccc aac agt gtt gat gag tcg tgg gat aac ttt ttt agg aat   343
Ala Asp Pro Asn Ser Val Asp Glu Ser Trp Asp Asn Phe Phe Arg Asn
            90                  95                  100

ttt gtg ggt cag gct tct aca tcg cct ggt atc tcg ggg caa acc att   391
Phe Val Gly Gln Ala Ser Thr Ser Pro Gly Ile Ser Gly Gln Thr Ile
        105                 110                 115

caa gaa agc atg cgt ttg ttg ttg cta gtt aga gct tac cag gtt aat   439
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Gln Glu Ser Met Arg Leu Leu Leu Leu Val Arg Ala Tyr Gln Val Asn
    120                 125                 130

ggc cac atg aag gcc aag ctt gat cct tta ggt cta gag aag aga gag    487
Gly His Met Lys Ala Lys Leu Asp Pro Leu Gly Leu Glu Lys Arg Glu
135                 140                 145                 150

att cca gag gat ctc acg cca ggt ctt tat ggg ttt act gag gct gat    535
Ile Pro Glu Asp Leu Thr Pro Gly Leu Tyr Gly Phe Thr Glu Ala Asp
                155                 160                 165

ctt gat cgg gaa ttc ttt ctg ggt gta tgg agg atg tcg ggt ttt ctc    583
Leu Asp Arg Glu Phe Phe Leu Gly Val Trp Arg Met Ser Gly Phe Leu
            170                 175                 180

tct gag aac cgc ccg gtt caa aca ctg agg tcg ata ctg tcg agg ctt    631
Ser Glu Asn Arg Pro Val Gln Thr Leu Arg Ser Ile Leu Ser Arg Leu
        185                 190                 195

gag caa gct tac tgt ggg act ata ggg tat gag tac atg cac att gct    679
Glu Gln Ala Tyr Cys Gly Thr Ile Gly Tyr Glu Tyr Met His Ile Ala
    200                 205                 210

gat agg gat aaa tgt aac tgg ttg aga gac aag atc gag acc cca act    727
Asp Arg Asp Lys Cys Asn Trp Leu Arg Asp Lys Ile Glu Thr Pro Thr
215                 220                 225                 230

cct cga cag tac aat agt gag cgt cgg atg gtt att tat gat agg ctt    775
Pro Arg Gln Tyr Asn Ser Glu Arg Arg Met Val Ile Tyr Asp Arg Leu
                235                 240                 245

acc tgg agc aca cag ttt gag aat ttc ttg gct act aag tgg acc acg    823
Thr Trp Ser Thr Gln Phe Glu Asn Phe Leu Ala Thr Lys Trp Thr Thr
            250                 255                 260

gct aaa agg ttt gga ctg gaa ggt gct gaa tct ttg att cct ggc atg    871
Ala Lys Arg Phe Gly Leu Glu Gly Ala Glu Ser Leu Ile Pro Gly Met
        265                 270                 275

aag gag atg ttc gat agg tct gca gat ctc ggg gta gag aac ata gtt    919
Lys Glu Met Phe Asp Arg Ser Ala Asp Leu Gly Val Glu Asn Ile Val
    280                 285                 290

atc ggt atg ccc cat agg ggt cga ctt aat gtt ttg ggt aat gtt gtt    967
Ile Gly Met Pro His Arg Gly Arg Leu Asn Val Leu Gly Asn Val Val
295                 300                 305                 310

aga aaa cct cta cgc caa ata ttc agc gag ttt agc ggt ggt act agg    1015
Arg Lys Pro Leu Arg Gln Ile Phe Ser Glu Phe Ser Gly Gly Thr Arg
                315                 320                 325

cca gta gat gaa gtt ggg ctt tac acc gga aca ggt gat gtg aaa tac    1063
Pro Val Asp Glu Val Gly Leu Tyr Thr Gly Thr Gly Asp Val Lys Tyr
            330                 335                 340

cac ttg ggt aca tct tat gat cgt cca act aga gga ggc aaa cat ctc    1111
His Leu Gly Thr Ser Tyr Asp Arg Pro Thr Arg Gly Gly Lys His Leu
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    345                 350                 355

cac ttg tct ttg gta gca aat ccc agt cac ttg gaa gca gta gat cct    1159
His Leu Ser Leu Val Ala Asn Pro Ser His Leu Glu Ala Val Asp Pro
    360                 365                 370

gtt gtg ata ggt aaa acc aga gcg aaa caa tat tac acg aaa gac gag    1207
Val Val Ile Gly Lys Thr Arg Ala Lys Gln Tyr Tyr Thr Lys Asp Glu
375                 380                 385                 390

aac aga aca aag aac atg ggt att ttg atc cat ggg gat ggt agc ttt    1255
Asn Arg Thr Lys Asn Met Gly Ile Leu Ile His Gly Asp Gly Ser Phe
                395                 400                 405

gcc gga caa gga gtg gtg tat gaa act ctc cat ctt agt gca ctt cct    1303
Ala Gly Gln Gly Val Val Tyr Glu Thr Leu His Leu Ser Ala Leu Pro
            410                 415                 420

aac tac tgt acc ggt gga aca gtg cac att gtg gtg aat aat caa gtg    1351
Asn Tyr Cys Thr Gly Gly Thr Val His Ile Val Val Asn Asn Gln Val
        425                 430                 435

gct ttc aca acc gat ccc agg gaa gga agg tct tca cag tat tgc act    1399
Ala Phe Thr Thr Asp Pro Arg Glu Gly Arg Ser Ser Gln Tyr Cys Thr
    440                 445                 450

gat gtt gca aag gct ttg agc gcc cca att ttc cat gtc aat gca gat    1447
Asp Val Ala Lys Ala Leu Ser Ala Pro Ile Phe His Val Asn Ala Asp
455                 460                 465                 470

gac att gaa gca gta gtg cat gct tgt gag ctt gct gct gag tgg cgc    1495
Asp Ile Glu Ala Val Val His Ala Cys Glu Leu Ala Ala Glu Trp Arg
                475                 480                 485

cag acg ttc cat tct gat gtt gtt gtt gat tta gta tgc tac cgt cgc    1543
Gln Thr Phe His Ser Asp Val Val Val Asp Leu Val Cys Tyr Arg Arg
            490                 495                 500

ttt ggg cat aac gag ata gac gaa ccg tca ttc aca caa cca aaa atg    1591
Phe Gly His Asn Glu Ile Asp Glu Pro Ser Phe Thr Gln Pro Lys Met
        505                 510                 515

tac aag gtctggctat tatatcatcc atctctgtga aataatctaa taaccaattc     1647
Tyr Lys
    520

aagtttccat ttcatacttt tcttgtactt ttttttgtt taaaaacgga tgttacttgt 1707

tggtgatag gtg ata cgc agt cat ccc tcg tca ctt caa atc tac cag gag 1758
          Val Ile Arg Ser His Pro Ser Ser Leu Gln Ile Tyr Gln Glu
                          525                 530

aag ctc ttg caa tct gga cag gta acc caa gaa gat att gat aag att    1806
Lys Leu Leu Gln Ser Gly Gln Val Thr Gln Glu Asp Ile Asp Lys Ile
535                 540                 545                 550

caa aag aaa gta agc tct atc ctc aat gaa gaa tat gag gca agt aaa    1854
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Gln Lys Lys Val Ser Ser Ile Leu Asn Glu Glu Tyr Glu Ala Ser Lys
                555                 560                 565

gat tat att cca caa aaa cgt gac tgg ctg gca agt cac tgg act gga   1902
Asp Tyr Ile Pro Gln Lys Arg Asp Trp Leu Ala Ser His Trp Thr Gly
            570                 575                 580

ttc aag tct ccg gag cag att tct agg att cga aac acc gg gtaaaaaaca 1953
Phe Lys Ser Pro Glu Gln Ile Ser Arg Ile Arg Asn Thr Gl
        585                 590                 595

tttttatttc atttagtttg tcaatgcctt ttggcctttt ttcttttctt tttcaatgta 2013

acattttgct ggaaaactat tcccttgttc ttttgcag a gtg aag cca gag att   2067
                                          y Val Lys Pro Glu Ile
                                                            600

ttg aag aat gtg gga aag gca atc tca acc ttc cct gag aac ttt aag   2115
Leu Lys Asn Val Gly Lys Ala Ile Ser Thr Phe Pro Glu Asn Phe Lys
            605                 610                 615

cca cac aga gga gtt aaa aga gtt tat gaa caa cgt gct caa atg att   2163
Pro His Arg Gly Val Lys Arg Val Tyr Glu Gln Arg Ala Gln Met Ile
        620                 625                 630

gaa tcg gga gaa ggc att gac tgg gga ctt gga gaa gca ctt gct ttt   2211
Glu Ser Gly Glu Gly Ile Asp Trp Gly Leu Gly Glu Ala Leu Ala Phe
    635                 640                 645

gct aca ctg gtt gtg gaa ggg aac cat gtt cgg cta agt ggt caa gat   2259
Ala Thr Leu Val Val Glu Gly Asn His Val Arg Leu Ser Gly Gln Asp
650                 655                 660                 665

gtt gaa aga gga act ttc agt cat aga cac tca gtg ctt cat gat caa   2307
Val Glu Arg Gly Thr Phe Ser His Arg His Ser Val Leu His Asp Gln
                670                 675                 680

gaa acc ggg gag gaa tat tgt ccc ctc gat cac cta atc aaa aac caa   2355
Glu Thr Gly Glu Glu Tyr Cys Pro Leu Asp His Leu Ile Lys Asn Gln
            685                 690                 695

gac cct gaa atg ttc act gtc agc aac ag gtatgcattt tttttaatc       2404
Asp Pro Glu Met Phe Thr Val Ser Asn Se
        700                 705

tctagagatg ataaccactc ttcaattgtt tttacatgat ctttacgttg tttgtgtatg 2464

cag c tcc ctt tca gaa ttt ggt gtt ctc ggt ttc gaa ctg ggt tat tcg 2513
      r Ser Leu Ser Glu Phe Gly Val Leu Gly Phe Glu Leu Gly Tyr Se
              710                 715                 720

atg gaa aat ccc aat tct ctg gtg ata tgg gaa gct cag ttt gga gac   2561
r Met Glu Asn Pro Asn Ser Leu Val Ile Trp Glu Ala Gln Phe Gly As
          725                 730                 735

ttt gct aat ggc gca caa gtt atg ttt gat cag ttc ata agc agt ggg   2609
p Phe Ala Asn Gly Ala Gln Val Met Phe Asp Gln Phe Ile Ser Ser Gl
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        740                 745                 750

gaa gcc aaa tgg ctc cgt caa act ggt cta gta gtt tta ctt cct cat   2657
y Glu Ala Lys Trp Leu Arg Gln Thr Gly Leu Val Val Leu Leu Pro Hi
755                 760                 765                 770

gga tat gat ggt cag ggt cct gaa cat tcc agt gga aga ttg gaa cgt   2705
s Gly Tyr Asp Gly Gln Gly Pro Glu His Ser Ser Gly Arg Leu Glu Ar
                775                 780                 785

ttc ctt cag gtatattata tgaccgatac ttaccgttaa gattctctcc           2754
g Phe Leu Gln

acttttgta tttgtttccc tctcatttga aaattttaac tgcag atg agt gat gac 2811
                                                 Met Ser Asp As
                                                 790

aat cct tac gtt atc cct gag atg gac cca act ctt cga aag cag att   2859
p Asn Pro Tyr Val Ile Pro Glu Met Asp Pro Thr Leu Arg Lys Gln Il
      795                 800                 805

caa gaa tgt aat tgg caa gtt gtt aat gtt act aca cct gcc aac tat   2907
e Gln Glu Cys Asn Trp Gln Val Val Asn Val Thr Thr Pro Ala Asn Ty
810                 815                 820                 825

ttc cat gtt ctg cgt cgg cag gtaaaatatc tatttatccc aagttcgtaa      2958
r Phe His Val Leu Arg Arg Gln
                830

aatgttgtta cttaattttc gtattcttca cactcacatg cttgatatca tccatttgca 3018

g ata cac agg gac ttt cgc aag cct ctt ata gtg atg gcc ccc aaa aac 3067
  Ile His Arg Asp Phe Arg Lys Pro Leu Ile Val Met Ala Pro Lys As
          835                 840                 845

ttg ctt cgt cac aaa cag tgt gta tct aat ctc tcg gaa ttc gat gat   3115
n Leu Leu Arg His Lys Gln Cys Val Ser Asn Leu Ser Glu Phe Asp As
      850                 855                 860

gtt aaa gga cat cct gga ttt gac aag caa gga act cga ttt aaa cgg   3163
p Val Lys Gly His Pro Gly Phe Asp Lys Gln Gly Thr Arg Phe Lys Ar
865                 870                 875                 880

ttg atc aaa gat caa agt ggc cac tct gat ctt gaa gaa g gtatcagacg  3213
g Leu Ile Lys Asp Gln Ser Gly His Ser Asp Leu Glu Glu     A
                885                 890

tctagtcctc tgctctggga aggtataaaa aaaaagatcc actttttccg tcattaacta 3273

acaaagttcc cacattctga aatttaatac tttaaatgtc aatgaatcag gtctactatg 3333

agcttgacga agagcgaaag aagtctgaaa caaaggatgt agccatttgc agagtagagc 3393

agctttgccc atttccatat gatctcatcc aaagagaact aaagcgatat ccaagtaggc 3453

gtcgaaaact caagtttgtg ttcaatagtt ttggttgatt atggaattct ttgaaacttt 3513
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tgttcttgtg tttaacag at gca gag atc gtg tgg tgt caa gaa gag ccg 3563
sp Ala Glu Ile Val Trp Cys Gln Glu Glu Pro
895 900

atg aac atg gga gga tac caa tac ata gcc cta agg ctt tgc acc gcg 3611
Met Asn Met Gly Gly Tyr Gln Tyr Ile Ala Leu Arg Leu Cys Thr Ala
905 910 915

atg aaa gca ctg caa aga gga aac ttc aac gac atc aaa tac gtt ggt 3659
Met Lys Ala Leu Gln Arg Gly Asn Phe Asn Asp Ile Lys Tyr Val Gly
920 925 930 935

cgt ctt ccc tca gct gct aca gcc aca gga ttt tac cag ctt cat gtt 3707
Arg Leu Pro Ser Ala Ala Thr Ala Thr Gly Phe Tyr Gln Leu His Val
940 945 950

aag gag cag act gat ctt gtg aag aaa gct ctt caa cct gac ccc atc 3755
Lys Glu Gln Thr Asp Leu Val Lys Lys Ala Leu Gln Pro Asp Pro Ile
955 960 965

acc ccc gtc atc cct taa aaaaacacag cttgaga 3790
Thr Pro Val Ile Pro
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Val Leu Pro Cys Gln Thr Arg Cys Phe His Ser Thr Ile Leu Lys Ser
35 40 45

Lys Ala Glu Ser Ala Ala Pro Val Pro Arg Pro Val Pro Leu Ser Lys
50 55 60

Leu Thr Asp Ser Phe Leu Asp Gly Thr Ser Ser Val Tyr Leu Glu Glu
65 70 75 80

Leu Gln Arg Ala Trp Glu Ala Asp Pro Asn Ser Val Asp Glu Ser Trp
85 90 95

Asp Asn Phe Phe Arg Asn Phe Val Gly Gln Ala Ser Thr Ser Pro Gly
100 105 110

Ile Ser Gly Gln Thr Ile Gln Glu Ser Met Arg Leu Leu Leu Leu Val
115 120 125

Arg Ala Tyr Gln Val Asn Gly His Met Lys Ala Lys Leu Asp Pro Leu
130 135 140

Gly Leu Glu Lys Arg Glu Ile Pro Glu Asp Leu Thr Pro Gly Leu Tyr
145 150 155 160

Gly Phe Thr Glu Ala Asp Leu Asp Arg Glu Phe Phe Leu Gly Val Trp
165 170 175

Arg Met Ser Gly Phe Leu Ser Glu Asn Arg Pro Val Gln Thr Leu Arg
180 185 190

Ser Ile Leu Ser Arg Leu Glu Gln Ala Tyr Cys Gly Thr Ile Gly Tyr
195 200 205

Glu Tyr Met His Ile Ala Asp Arg Asp Lys Cys Asn Trp Leu Arg Asp
210 215 220

Lys Ile Glu Thr Pro Thr Pro Arg Gln Tyr Asn Ser Glu Arg Arg Met
225 230 235 240

Val Ile Tyr Asp Arg Leu Thr Trp Ser Thr Gln Phe Glu Asn Phe Leu
245 250 255

Ala Thr Lys Trp Thr Thr Ala Lys Arg Phe Gly Leu Glu Gly Ala Glu
260 265 270

Ser Leu Ile Pro Gly Met Lys Glu Met Phe Asp Arg Ser Ala Asp Leu
275 280 285

Gly Val Glu Asn Ile Val Ile Gly Met Pro His Arg Gly Arg Leu Asn
290 295 300

Val Leu Gly Asn Val Val Arg Lys Pro Leu Arg Gln Ile Phe Ser Glu
305 310 315 320

Phe Ser Gly Gly Thr Arg Pro Val Asp Glu Val Gly Leu Tyr Thr Gly
325 330 335

Thr Gly Asp Val Lys Tyr His Leu Gly Thr Ser Tyr Asp Arg Pro Thr
340 345 350

Arg Gly Gly Lys His Leu His Leu Ser Leu Val Ala Asn Pro Ser His
355 360 365

Leu Glu Ala Val Asp Pro Val Val Ile Gly Lys Thr Arg Ala Lys Gln
370 375 380

Tyr Tyr Thr Lys Asp Glu Asn Arg Thr Lys Asn Met Gly Ile Leu Ile
385 390 395 400

His Gly Asp Gly Ser Phe Ala Gly Gln Gly Val Val Tyr Glu Thr Leu
405 410 415

His Leu Ser Ala Leu Pro Asn Tyr Cys Thr Gly Gly Thr Val His Ile
420 425 430

Val Val Asn Asn Gln Val Ala Phe Thr Thr Asp Pro Arg Glu Gly Arg
435 440 445

Ser Ser Gln Tyr Cys Thr Asp Val Ala Lys Ala Leu Ser Ala Pro Ile
450 455 460

Phe His Val Asn Ala Asp Asp Ile Glu Ala Val Val His Ala Cys Glu
465 470 475 480

Leu Ala Ala Glu Trp Arg Gln Thr Phe His Ser Asp Val Val Val Asp
485 490 495

Leu Val Cys Tyr Arg Arg Phe Gly His Asn Glu Ile Asp Glu Pro Ser
500 505 510

Phe Thr Gln Pro Lys Met Tyr Lys Val Ile Arg Ser His Pro Ser Ser
515 520 525

Leu Gln Ile Tyr Gln Glu Lys Leu Leu Gln Ser Gly Gln Val Thr Gln
530 535 540

Glu Asp Ile Asp Lys Ile Gln Lys Lys Val Ser Ser Ile Leu Asn Glu
545 550 555 560

Glu Tyr Glu Ala Ser Lys Asp Tyr Ile Pro Gln Lys Arg Asp Trp Leu
565 570 575

Ala Ser His Trp Thr Gly Phe Lys Ser Pro Glu Gln Ile Ser Arg Ile
580 585 590

Arg Asn Thr Gly Val Lys Pro Glu Ile Leu Lys Asn Val Gly Lys Ala
595 600 605

Ile Ser Thr Phe Pro Glu Asn Phe Lys Pro His Arg Gly Val Lys Arg
610 615 620

Val Tyr Glu Gln Arg Ala Gln Met Ile Glu Ser Gly Glu Gly Ile Asp
625 630 635 640

Trp Gly Leu Gly Glu Ala Leu Ala Phe Ala Thr Leu Val Val Glu Gly
645 650 655

Asn His Val Arg Leu Ser Gly Gln Asp Val Glu Arg Gly Thr Phe Ser
660 665 670

His Arg His Ser Val Leu His Asp Gln Glu Thr Gly Glu Glu Tyr Cys
675 680 685

Pro Leu Asp His Leu Ile Lys Asn Gln Asp Pro Glu Met Phe Thr Val
690 695 700

Ser Asn Ser Ser Leu Ser Glu Phe Gly Val Leu Gly Phe Glu Leu
705 710 715 720

Gly Tyr Ser Met Glu Asn Pro Asn Ser Leu Val Ile Trp Glu Ala Gln
725 730 73

Phe Gly Ap Phe Ala Asn Gly Ala Gln Val Met Phe Asp Gln Phe Ile
740 745 750

Ser Ser Gy Glu Ala Lys Trp Leu Arg Gln Thr Gly Leu Val Val Leu
755 760 765

Leu Pro Hs Gly Tyr Asp Gly Gln Gly Pro Glu His Ser Ser Gly Arg
770 775 780

Leu Glu Ag Phe Leu Gln Met Ser Asp Asp Asn Pro Tyr Val Ile Pro
785 790 795

Glu Met Asp Pro Thr Leu Arg Lys Gln Ile Gln Glu Cys Asn Trp Gln
800 805 810

Val Val Asn Val Thr Thr Pro Ala Asn Trp Phe His Val Leu Arg Arg
815 820 825

Gln Ile His Arg Asp Phe Arg Lys Pro Leu Ile Val Met Ala Pro Lys
830 835 840

Asn Leu Leu Arg His Lys Gln Cys Val Ser Asn Leu Ser Glu Phe Asp
845 850 855

Asp Val Lys Gly His Pro Gly Phe Asp Lys Gln Gly Thr Arg Phe Lys
860 865 870

Arg Leu Ile Lys Asp Gln Ser Gly His Ser Asp Leu Glu Glu
875 880 885

Asp Ala Glu Ile Val Trp Cys Gln Glu Glu Pro Met Asn Met Gly Gly
890 895 900

Tyr Gln Tyr Ile Ala Leu Arg Leu Cys Thr Ala Met Lys Ala Leu Gln
905 910 915

Arg Gly Asn Phe Asn Asp Ile Lys Tyr Val Gly Arg Leu Pro Ser Ala
920 925 930

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935

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                            1               5

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Ala Thr Phe Val Glu Asp Phe Lys Ala Ala Trp Ser Glu Ser His Ile
 10                 15                  20                  25

cgt caa atg gaa gac gga aaa gct atc cag ctc gtc ctt gat cag agc   147
Arg Gln Met Glu Asp Gly Lys Ala Ile Gln Leu Val Leu Asp Gln Ser
                30                  35                  40

act g gtacaccaac gccacagtta tatttttaaa cggaaacatt ttgaaattaa      201
Thr G

tggtgttttt atgtaatata ctctcactgt acatgttcat atttgtcttt taaag ga   258
                                                             ly

tgt gga ttt gct tcc aaa aga aaa tat cta ttc gga cga gtg agc atg   306
Cys Gly Phe Ala Ser Lys Arg Lys Tyr Leu Phe Gly Arg Val Ser Met
     45                  50                  55

aag atc aaa ctc att ccc gga gac tct gcc ggt acg gtc acc gct ttc   354
Lys Ile Lys Leu Ile Pro Gly Asp Ser Ala Gly Thr Val Thr Ala Phe
 60                  65                  70                  75

tac gtaagtctat cattttactc cactagtttt gaaattttac acattcacac         407
Tyr

aataaaaaat aacattttct tgaaacacta acggtcaaat cattgatatg tctatag     464

atg aac tcc gat acg gcc acg gtg aga gac gag cta gat ttt gag ttc   512
Met Asn Ser Asp Thr Ala Thr Val Arg Asp Glu Leu Asp Phe Glu Phe
                80                  85                  90

ttg gga aac aga agt ggt caa cct tac tca gtg caa aca aac ata ttt   560
Leu Gly Asn Arg Ser Gly Gln Pro Tyr Ser Val Gln Thr Asn Ile Phe
             95                 100                 105

gct cat ggc aaa gga gat aga gaa caa aga gtt aat ctt tgg ttc gac   608
Ala His Gly Lys Gly Asp Arg Glu Gln Arg Val Asn Leu Trp Phe Asp
    110                 115                 120

cca tct atg gat tac cac act tac act atc tta tgg tca cac aaa cac   656
Pro Ser Met Asp Tyr His Thr Tyr Thr Ile Leu Trp Ser His Lys His
125                 130                 135                 140
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att gtg taagcttttc tctaattgta ctttcaacta gaatcaacat ttactgtttc    712
Ile Val

aaaacaaaaa atcaccattt actgtttaaa aaaaccttag tttaacgtgg ggttgttttg 772

gttactcagt ttt tac gta gac gat gtg cca ata aga gaa tac aaa aac    821
           Phe Tyr Val Asp Asp Val Pro Ile Arg Glu Tyr Lys Asn
                   145                 150                 155

aac gaa gcc aag aac ata gct tac cca aca tca caa cct atg gga gta   869
Asn Glu Ala Lys Asn Ile Ala Tyr Pro Thr Ser Gln Pro Met Gly Val
                160                 165                 170

tac tca aca tta tgg gaa gca gat gac tgg gca aca cgt ggt gga tta   917
Tyr Ser Thr Leu Trp Glu Ala Asp Asp Trp Ala Thr Arg Gly Gly Leu
            175                 180                 185

gag aaa att gat tgg agc aaa gct cca ttt tat gct tat tac aaa gat   965
Glu Lys Ile Asp Trp Ser Lys Ala Pro Phe Tyr Ala Tyr Tyr Lys Asp
        190                 195                 200

ttc gac atc gaa ggt tgt cct gtt cct gga cca acc ttt tgt cca tcg   1013
Phe Asp Ile Glu Gly Cys Pro Val Pro Gly Pro Thr Phe Cys Pro Ser
    205                 210                 215

aac cct cat aat tgg tgg gaa ggt tat gcc tat cag tct ctt aac gcc   1061
Asn Pro His Asn Trp Trp Glu Gly Tyr Ala Tyr Gln Ser Leu Asn Ala
220                 225                 230                 235

gtt gaa gct cga cgt tac cgg tgg gtt aga gta aac cat atg gtt tat   1109
Val Glu Ala Arg Arg Tyr Arg Trp Val Arg Val Asn His Met Val Tyr
                240                 245                 250

gat tat tgt act gac cgg tct agg ttt cct gtc cca cca ccc gag tgt   1157
Asp Tyr Cys Thr Asp Arg Ser Arg Phe Pro Val Pro Pro Pro Glu Cys
            255                 260                 265

cgt gct tga aaataattgc atacgtacgt tgcaatgatc atgt                 1200
Arg Ala
        270


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&lt;213&gt; Arabidopsis thaliana

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Ala Ile Gln Leu Val Leu Asp Gln Ser Thr Gly Cys Gly Phe Ala Ser
        35                  40                  45
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Lys Arg Lys Tyr Leu Phe Gly Arg Val Ser Met Lys Ile Lys Leu Ile
50 55 60

Pro Gly Asp Ser Ala Gly Thr Val Thr Ala Phe Tyr Met Asn Ser Asp
65 70 75 80

Thr Ala Thr Val Arg Asp Glu Leu Asp Phe Glu Phe Leu Gly Asn Arg
85 90 95

Ser Gly Gln Pro Tyr Ser Val Gln Thr Asn Ile Phe Ala His Gly Lys
100 105 110

Gly Asp Arg Glu Gln Arg Val Asn Leu Trp Phe Asp Pro Ser Met Asp
115 120 125

Tyr His Thr Tyr Thr Ile Leu Trp Ser His Lys His Ile Val Phe Tyr
130 135 140

Val Asp Asp Val Pro Ile Arg Glu Tyr Lys Asn Asn Glu Ala Lys Asn
145 150 155 160

Ile Ala Tyr Pro Thr Ser Gln Pro Met Gly Val Tyr Ser Thr Leu Trp
165 170 175

Glu Ala Asp Asp Trp Ala Thr Arg Gly Gly Leu Glu Lys Ile Asp Trp
180 185 190

Ser Lys Ala Pro Phe Tyr Ala Tyr Tyr Lys Asp Phe Asp Ile Glu Gly
195 200 205

Cys Pro Val Pro Gly Pro Thr Phe Cys Pro Ser Asn Pro His Asn Trp
210 215 220

Trp Glu Gly Tyr Ala Tyr Gln Ser Leu Asn Ala Val Glu Ala Arg Arg
225 230 235 240

Tyr Arg Trp Val Arg Val Asn His Met Val Tyr Asp Tyr Cys Thr Asp
245 250 255

Arg Ser Arg Phe Pro Val Pro Pro Pro Glu Cys Arg Ala
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atc cgc aga acc cta acc aaa cca cac ggc act ttt tcc cgg tgt cgc     99
Ile Arg Arg Thr Leu Thr Lys Pro His Gly Thr Phe Ser Arg Cys Arg
 10                  15                  20                  25

tac tta tca acc gcc gct gct gcg acg gag gtg aat tac gag gat gaa    147
Tyr Leu Ser Thr Ala Ala Ala Ala Thr Glu Val Asn Tyr Glu Asp Glu
                 30                  35                  40

tcg att atg atg aaa gga gtt cga att tca ggt aga cct ctt tac tta    195
Ser Ile Met Met Lys Gly Val Arg Ile Ser Gly Arg Pro Leu Tyr Leu
             45                  50                  55

gat atg caa gcg acg act ccg att gat cct aga gta ttc gat gcg atg    243
Asp Met Gln Ala Thr Thr Pro Ile Asp Pro Arg Val Phe Asp Ala Met
         60                  65                  70

aat gct tca cag atc cat gag tat ggg aat cct cac tcg cga acg cat    291
Asn Ala Ser Gln Ile His Glu Tyr Gly Asn Pro His Ser Arg Thr His
     75                  80                  85

ctc tac ggc tgg gaa gct gag aac gcc gtc gag aac gca cga aac cag    339
Leu Tyr Gly Trp Glu Ala Glu Asn Ala Val Glu Asn Ala Arg Asn Gln
 90                  95                 100                 105

gtc gcg aaa ctg atc gaa gct tca ccg aag gag atc gta ttc gtg tcc    387
Val Ala Lys Leu Ile Glu Ala Ser Pro Lys Glu Ile Val Phe Val Ser
                110                 115                 120

ggt gca acg gag gcg aac aat atg gcg gtg aaa gga gtg atg cac ttt    435
Gly Ala Thr Glu Ala Asn Asn Met Ala Val Lys Gly Val Met His Phe
            125                 130                 135

tac aag gac acg aag aaa cat gtg ata act aca cag act gag cat aag    483
Tyr Lys Asp Thr Lys Lys His Val Ile Thr Thr Gln Thr Glu His Lys
        140                 145                 150

tgt gtg ctt gat tcg tgt agg cat ttg cag caa gaa gga ttt gag gta    531
Cys Val Leu Asp Ser Cys Arg His Leu Gln Gln Glu Gly Phe Glu Val
    155                 160                 165

act tat tta cct gtg aaa act gat gga ttg gtt gat tta gag atg ttg    579
Thr Tyr Leu Pro Val Lys Thr Asp Gly Leu Val Asp Leu Glu Met Leu
170                 175                 180                 185

aga gaa gct att agg cca gac aca ggg cta gtt tct att atg gct gtg    627
Arg Glu Ala Ile Arg Pro Asp Thr Gly Leu Val Ser Ile Met Ala Val
                190                 195                 200

aac aat gag att ggt gtg gtt caa cct atg gag gag att ggt atg att    675
Asn Asn Glu Ile Gly Val Val Gln Pro Met Glu Glu Ile Gly Met Ile
            205                 210                 215
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tgc aaa gag cat aat gtt ccg ttt cat act gat gct gct caa gct att     723
Cys Lys Glu His Asn Val Pro Phe His Thr Asp Ala Ala Gln Ala Ile
        220                 225                 230

ggg aag ata cct gtt gat gtt aag aag tgg aat gtt gct ttg atg tct     771
Gly Lys Ile Pro Val Asp Val Lys Lys Trp Asn Val Ala Leu Met Ser
    235                 240                 245

atg agt gct cac aag atc tat gga ccg aaa ggt gtt ggt gct ttg tat     819
Met Ser Ala His Lys Ile Tyr Gly Pro Lys Gly Val Gly Ala Leu Tyr
250                 255                 260                 265

gtg agg agg agg ccg aga atc agg ctt gag ccg ttg atg aat ggt gga     867
Val Arg Arg Arg Pro Arg Ile Arg Leu Glu Pro Leu Met Asn Gly Gly
                270                 275                 280

ggt cag gag agg gga ttg cgt agt ggt acg ggg gct acg cag cag att     915
Gly Gln Glu Arg Gly Leu Arg Ser Gly Thr Gly Ala Thr Gln Gln Ile
            285                 290                 295

gtt ggg ttc ggg gct gct tgt gag ttg gct atg aag gag atg gag tat     963
Val Gly Phe Gly Ala Ala Cys Glu Leu Ala Met Lys Glu Met Glu Tyr
        300                 305                 310

gat gag aag tgg att aag ggg tta cag gag agg ttg ctg aat ggg gtt     1011
Asp Glu Lys Trp Ile Lys Gly Leu Gln Glu Arg Leu Leu Asn Gly Val
    315                 320                 325

aga gag aag ctt gat ggt gtt gtg gtg aat ggt tca atg gat agt cga     1059
Arg Glu Lys Leu Asp Gly Val Val Val Asn Gly Ser Met Asp Ser Arg
330                 335                 340                 345

tat gta ggg aat ttg aat ttg tcg ttt gct tat gtt gaa gga gag agt     1107
Tyr Val Gly Asn Leu Asn Leu Ser Phe Ala Tyr Val Glu Gly Glu Ser
                350                 355                 360

ttg ttg atg gga ttg aag gaa gtt gca gtg tct agt gga agt gct tgt     1155
Leu Leu Met Gly Leu Lys Glu Val Ala Val Ser Ser Gly Ser Ala Cys
            365                 370                 375

act agt gcg agt ttg gag cct tct tat gtg ttg aga gct ttg ggt gtg     1203
Thr Ser Ala Ser Leu Glu Pro Ser Tyr Val Leu Arg Ala Leu Gly Val
        380                 385                 390

gat gaa gac atg gct cac act tcg att agg ttt ggg att ggt agg ttt     1251
Asp Glu Asp Met Ala His Thr Ser Ile Arg Phe Gly Ile Gly Arg Phe
    395                 400                 405

acc acg aag gaa gag att gat aaa gcg gtc gag ctt acg gtt aaa caa     1299
Thr Thr Lys Glu Glu Ile Asp Lys Ala Val Glu Leu Thr Val Lys Gln
410                 415                 420                 425

gtt gag aag ttg agg gaa atg agc ccg ctt tat gaa atg gtt aaa gaa     1347
Val Glu Lys Leu Arg Glu Met Ser Pro Leu Tyr Glu Met Val Lys Glu
                430                 435                 440

ggt atc gat atc aag aac att caa tgg tct caa cac tga ttcaacagtt      1396
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cca 1399

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35 40 45

Arg Ile Ser Gly Arg Pro Leu Tyr Leu Asp Met Gln Ala Thr Thr Pro
50 55 60

Ile Asp Pro Arg Val Phe Asp Ala Met Asn Ala Ser Gln Ile His Glu
65 70 75 80

Tyr Gly Asn Pro His Ser Arg Thr His Leu Tyr Gly Trp Glu Ala Glu
85 90 95

Asn Ala Val Glu Asn Ala Arg Asn Gln Val Ala Lys Leu Ile Glu Ala
100 105 110

Ser Pro Lys Glu Ile Val Phe Val Ser Gly Ala Thr Glu Ala Asn Asn
115 120 125

Met Ala Val Lys Gly Val Met His Phe Tyr Lys Asp Thr Lys Lys His
130 135 140

Val Ile Thr Thr Gln Thr Glu His Lys Cys Val Leu Asp Ser Cys Arg
145 150 155 160

His Leu Gln Gln Glu Gly Phe Glu Val Thr Tyr Leu Pro Val Lys Thr
165 170 175

Asp Gly Leu Val Asp Leu Glu Met Leu Arg Glu Ala Ile Arg Pro Asp
180 185 190

Thr Gly Leu Val Ser Ile Met Ala Val Asn Asn Glu Ile Gly Val Val
195 200 205

Gln Pro Met Glu Glu Ile Gly Met Ile Cys Lys Glu His Asn Val Pro
210 215 220

Phe His Thr Asp Ala Ala Gln Ala Ile Gly Lys Ile Pro Val Asp Val
225 230 235 240

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Lys Lys Trp Asn Val Ala Leu Met Ser Met Ser Ala His Lys Ile Tyr
                245                 250                 255

Gly Pro Lys Gly Val Gly Ala Leu Tyr Val Arg Arg Arg Pro Arg Ile
            260                 265                 270

Arg Leu Glu Pro Leu Met Asn Gly Gly Gly Gln Glu Arg Gly Leu Arg
        275                 280                 285

Ser Gly Thr Gly Ala Thr Gln Gln Ile Val Gly Phe Gly Ala Ala Cys
    290                 295                 300

Glu Leu Ala Met Lys Glu Met Glu Tyr Asp Glu Lys Trp Ile Lys Gly
305                 310                 315                 320

Leu Gln Glu Arg Leu Leu Asn Gly Val Arg Glu Lys Leu Asp Gly Val
                325                 330                 335

Val Val Asn Gly Ser Met Asp Ser Arg Tyr Val Gly Asn Leu Asn Leu
            340                 345                 350

Ser Phe Ala Tyr Val Glu Gly Glu Ser Leu Leu Met Gly Leu Lys Glu
        355                 360                 365

Val Ala Val Ser Ser Gly Ser Ala Cys Thr Ser Ala Ser Leu Glu Pro
    370                 375                 380

Ser Tyr Val Leu Arg Ala Leu Gly Val Asp Glu Asp Met Ala His Thr
385                 390                 395                 400

Ser Ile Arg Phe Gly Ile Gly Arg Phe Thr Thr Lys Glu Glu Ile Asp
                405                 410                 415

Lys Ala Val Glu Leu Thr Val Lys Gln Val Glu Lys Leu Arg Glu Met
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Ser Pro Leu Tyr Glu Met Val Lys Glu Gly Ile Asp Ile Lys Asn Ile
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ctt ctt tct tgt ttt ctc caa gtt tct tcc aat gga gac gct gag ata 97
Leu Leu Ser Cys Phe Leu Gln Val Ser Ser Asn Gly Asp Ala Glu Ile
15 20 25 30

ttg agt aga gtt aaa aag acc cga ctt ttc gac ccc gat gga aat tta 145
Leu Ser Arg Val Lys Lys Thr Arg Leu Phe Asp Pro Asp Gly Asn Leu
35 40 45

caa gat tgg gtc ata acc gga gat aat cgg agt cca tgt aat tgg acg 193
Gln Asp Trp Val Ile Thr Gly Asp Asn Arg Ser Pro Cys Asn Trp Thr
50 55 60

gga atc aca tgc cac atc aga aaa ggt agc tcc ctc gcc gtc act acc 241
Gly Ile Thr Cys His Ile Arg Lys Gly Ser Ser Leu Ala Val Thr Thr
65 70 75

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Ile Asp Leu Ser Gly Tyr Asn Ile Ser Gly Gly Phe Pro Tyr Gly Phe
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Cys Arg Ile Arg Thr Leu Ile Asn Ile Thr Leu Ser Gln Asn Asn Leu
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aat ggt acg att gat tct gct cct ctc tcc ctc tgt tct aaa ctt cag 385
Asn Gly Thr Ile Asp Ser Ala Pro Leu Ser Leu Cys Ser Lys Leu Gln
115 120 125

aat ttg att ctc aat caa aac aac ttc tcc ggt aaa tta ccg gaa ttc 433
Asn Leu Ile Leu Asn Gln Asn Asn Phe Ser Gly Lys Leu Pro Glu Phe
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Ser Pro Glu Phe Arg Lys Leu Arg Val Leu Glu Leu Glu Ser Asn Leu
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Phe Thr Gly Glu Ile Pro Gln Ser Tyr Gly Arg Leu Thr Ala Leu Gln
160 165 170

gtt ctg aat ctt aat ggt aac ccg ctc agt gga atc gtt ccg gcg ttt 577
Val Leu Asn Leu Asn Gly Asn Pro Leu Ser Gly Ile Val Pro Ala Phe
175 180 185 190

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Leu Gly Tyr Leu Thr Glu Leu Thr Arg Leu Asp Leu Ala Tyr Ile Ser
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Phe Asp Pro Ser Pro Ile Pro Ser Thr Leu Gly Asn Leu Ser Asn Leu
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act gat ctt cgg cta act cac tcg aac ctc gtc gga gaa att cct gat     721
Thr Asp Leu Arg Leu Thr His Ser Asn Leu Val Gly Glu Ile Pro Asp
        225                 230                 235

tcg atc atg aat ctg gtg ttg tta gag aat ctt gat tta gct atg aat     769
Ser Ile Met Asn Leu Val Leu Leu Glu Asn Leu Asp Leu Ala Met Asn
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agt ctc acc gga gaa ata cct gag agt atc gga aga ctc gaa tcg gtt     817
Ser Leu Thr Gly Glu Ile Pro Glu Ser Ile Gly Arg Leu Glu Ser Val
255                 260                 265                 270

tac cag att gag ctc tac gat aac cgg tta tct gga aaa tta ccg gag     865
Tyr Gln Ile Glu Leu Tyr Asp Asn Arg Leu Ser Gly Lys Leu Pro Glu
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agt atc gga aat tta acc gaa ttg agg aat ttt gat gtc tcg cag aat     913
Ser Ile Gly Asn Leu Thr Glu Leu Arg Asn Phe Asp Val Ser Gln Asn
            290                 295                 300

aat cta acc ggt gaa cta ccg gaa aag atc gct gct ctg caa ctt atc     961
Asn Leu Thr Gly Glu Leu Pro Glu Lys Ile Ala Ala Leu Gln Leu Ile
        305                 310                 315

tct ttc aat ctc aat gat aat ttc ttc acc gga gga tta cca gat gtc    1009
Ser Phe Asn Leu Asn Asp Asn Phe Phe Thr Gly Gly Leu Pro Asp Val
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gta gct ttg aat cct aat ctc gtt gaa ttc aaa atc ttc aac aac agt    1057
Val Ala Leu Asn Pro Asn Leu Val Glu Phe Lys Ile Phe Asn Asn Ser
335                 340                 345                 350

ttc acg ggg acg tta cca agg aat ctc ggg aaa ttc tca gaa atc tct    1105
Phe Thr Gly Thr Leu Pro Arg Asn Leu Gly Lys Phe Ser Glu Ile Ser
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gaa ttc gat gtc tcg acg aac aga ttc tcc ggt gaa ttg ccg ccg tat    1153
Glu Phe Asp Val Ser Thr Asn Arg Phe Ser Gly Glu Leu Pro Pro Tyr
            370                 375                 380

ttg tgc tac aga aga aaa ctt cag aag att atc acc ttc agc aat caa    1201
Leu Cys Tyr Arg Arg Lys Leu Gln Lys Ile Ile Thr Phe Ser Asn Gln
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tta agc ggc gaa att ccg gaa tct tac ggc gat tgt cat tcg ctt aat    1249
Leu Ser Gly Glu Ile Pro Glu Ser Tyr Gly Asp Cys His Ser Leu Asn
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tac att cgt atg gcg gat aac aaa ctc tcc ggc gaa gtt ccg gct agg    1297
Tyr Ile Arg Met Ala Asp Asn Lys Leu Ser Gly Glu Val Pro Ala Arg
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ttt tgg gaa ctt cct ctt act cgt ctt gag cta gcc aac aac aat caa    1345
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Phe Trp Glu Leu Pro Leu Thr Arg Leu Glu Leu Ala Asn Asn Asn Gln
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tta caa ggt tcg att cct cct tcg att tcc aaa gct cgt cat cta tct   1393
Leu Gln Gly Ser Ile Pro Pro Ser Ile Ser Lys Ala Arg His Leu Ser
        450                 455                 460

cag ctt gaa atc tcc gct aac aac ttc tcc ggt gtg att ccc gtc aaa   1441
Gln Leu Glu Ile Ser Ala Asn Asn Phe Ser Gly Val Ile Pro Val Lys
    465                 470                 475

ctt tgt gat ctc cgt gat ctc aga gtc atc gat ctt agc cgc aac agt   1489
Leu Cys Asp Leu Arg Asp Leu Arg Val Ile Asp Leu Ser Arg Asn Ser
    480                 485                 490

ttc tta gga tca att ccg tct tgc atc aac aaa ttg aag aat cta gag   1537
Phe Leu Gly Ser Ile Pro Ser Cys Ile Asn Lys Leu Lys Asn Leu Glu
495                 500                 505                 510

aga gta gag atg cag gag aac atg ctc gac ggc gag att ccg agt tca   1585
Arg Val Glu Met Gln Glu Asn Met Leu Asp Gly Glu Ile Pro Ser Ser
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gtg agt tcg tgc acc gag tta acc gaa tta aat ctc tcc aac aac cgt   1633
Val Ser Ser Cys Thr Glu Leu Thr Glu Leu Asn Leu Ser Asn Asn Arg
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tta cga ggc ggg ata cca ccg gaa ctc ggt gat tta ccg gtt tta aac   1681
Leu Arg Gly Gly Ile Pro Pro Glu Leu Gly Asp Leu Pro Val Leu Asn
        545                 550                 555

tac ctg gat ctc tct aac aac caa ctc acc ggt gag att ccg gcg gag   1729
Tyr Leu Asp Leu Ser Asn Asn Gln Leu Thr Gly Glu Ile Pro Ala Glu
    560                 565                 570

ctg ttg agg ctc aag ctt aat caa ttc aac gtc tcc gat aac aaa ctc   1777
Leu Leu Arg Leu Lys Leu Asn Gln Phe Asn Val Ser Asp Asn Lys Leu
575                 580                 585                 590

tat g gtaagattcc ttctggattt cagcaagata tttttcgacc cagtttctta g gt 1834
Tyr G                                                          ly

aac ccg aat ctc tgt gcc cca aat ttg gat ccg att aga cct tgc cga   1882
Asn Pro Asn Leu Cys Ala Pro Asn Leu Asp Pro Ile Arg Pro Cys Arg
        595                 600                 605

tcc aaa cgg gaa acc cgg tac att ctc cca atc tca atc ctc tgc atc   1930
Ser Lys Arg Glu Thr Arg Tyr Ile Leu Pro Ile Ser Ile Leu Cys Ile
    610                 615                 620

gtt gca cta acc gga gct ttg gtt tgg cta ttc atc aaa acc aaa ccg   1978
Val Ala Leu Thr Gly Ala Leu Val Trp Leu Phe Ile Lys Thr Lys Pro
625                 630                 635                 640

tta ttc aag aga aaa ccg aaa cgg acc aac aaa ata acc atc ttc cag   2026
Leu Phe Lys Arg Lys Pro Lys Arg Thr Asn Lys Ile Thr Ile Phe Gln
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cgg gtc ggg ttc acg gag gaa gac ata tac ccg caa tta aca gaa gat    2074
Arg Val Gly Phe Thr Glu Glu Asp Ile Tyr Pro Gln Leu Thr Glu Asp
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aac ata att ggg tcg ggc ggg tcg ggt ttg gtt tat aga gtg aaa ctc    2122
Asn Ile Ile Gly Ser Gly Gly Ser Gly Leu Val Tyr Arg Val Lys Leu
        675                 680                 685

aaa tca ggt caa acg ctt gcg gtg aag aaa ctc tgg gga gaa acg ggt    2170
Lys Ser Gly Gln Thr Leu Ala Val Lys Lys Leu Trp Gly Glu Thr Gly
    690                 695                 700

caa aaa acg gaa tct gaa tct gtt ttt cga tcc gaa gta gag acg ttg    2218
Gln Lys Thr Glu Ser Glu Ser Val Phe Arg Ser Glu Val Glu Thr Leu
705                 710                 715                 720

ggt cgg gtc aga cat gga aac atc gtg aaa ctt ctt atg tgc tgc aac    2266
Gly Arg Val Arg His Gly Asn Ile Val Lys Leu Leu Met Cys Cys Asn
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ggc gag gag ttt cgg ttc tta gtg tac gag ttc atg gaa aac ggc agc    2314
Gly Glu Glu Phe Arg Phe Leu Val Tyr Glu Phe Met Glu Asn Gly Ser
            740                 745                 750

tta ggt gac gtt ttg cat tcg gag aaa gaa cat cgt gcc gtt tct cca    2362
Leu Gly Asp Val Leu His Ser Glu Lys Glu His Arg Ala Val Ser Pro
        755                 760                 765

ctt gat tgg acg aca cga ttt tcg atc gcg gtt ggt gct gct caa gga    2410
Leu Asp Trp Thr Thr Arg Phe Ser Ile Ala Val Gly Ala Ala Gln Gly
    770                 775                 780

ctt tct tat cta cat cat gac tct gtt ccg cct att gtt cac cgt gac    2458
Leu Ser Tyr Leu His His Asp Ser Val Pro Pro Ile Val His Arg Asp
785                 790                 795                 800

gtc aaa agc aat aat ata ttg ttg gac cat gag atg aag cca cgt gtc    2506
Val Lys Ser Asn Asn Ile Leu Leu Asp His Glu Met Lys Pro Arg Val
                805                 810                 815

gcc gat ttc ggt tta gct aaa ccg ttg aag aga gaa gac aat gat ggt    2554
Ala Asp Phe Gly Leu Ala Lys Pro Leu Lys Arg Glu Asp Asn Asp Gly
            820                 825                 830

gtc tcc gat gtt tca atg tct tgt gtt gct gga tcc tac ggc tac att    2602
Val Ser Asp Val Ser Met Ser Cys Val Ala Gly Ser Tyr Gly Tyr Ile
        835                 840                 845

gct ccg g gttcgaattc ttagctctac aatatcaaat cgttaaaacc ctatacgcaa   2659
Ala Pro G
    850

gcgttttagt aacattactg ttcttctgtg gatgcag aa tat ggt tat acg tca    2713
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aaa gtg aat gag aag agc gat gtc tat agc ttc ggg gtg gtt tta ctc   2761
Lys Val Asn Glu Lys Ser Asp Val Tyr Ser Phe Gly Val Val Leu Leu
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gaa ctg att acg gga aaa aga ccg aac gat tcg tct ttt ggg gag aat   2809
Glu Leu Ile Thr Gly Lys Arg Pro Asn Asp Ser Ser Phe Gly Glu Asn
        875                 880                 885

aag gac att gtt aag ttt gca atg gaa gca gct ttg tgt tac cct tct   2857
Lys Asp Ile Val Lys Phe Ala Met Glu Ala Ala Leu Cys Tyr Pro Ser
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cca tca gca gaa gac gga gcc atg aat caa gat tca ctt gga aac tat   2905
Pro Ser Ala Glu Asp Gly Ala Met Asn Gln Asp Ser Leu Gly Asn Tyr
905                 910                 915                 920

cga gat ctt agc aag ctt gtt gat cca aag atg aaa ctt tcg acg aga   2953
Arg Asp Leu Ser Lys Leu Val Asp Pro Lys Met Lys Leu Ser Thr Arg
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gag tat gaa gag ata gag aaa gtt ctt gac gtt gca ttg ctc tgt acg   3001
Glu Tyr Glu Glu Ile Glu Lys Val Leu Asp Val Ala Leu Leu Cys Thr
            940                 945                 950

tcg tct ttt cct atc aac agg ccg acc atg agg aaa gta gta gag ttg   3049
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Arg Val Lys Lys Thr Arg Leu Phe Asp Pro Asp Gly Asn Leu Gln Asp
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Trp Val Ile Thr Gly Asp Asn Arg Ser Pro Cys Asn Trp Thr Gly Ile
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Thr Cys His Ile Arg Lys Gly Ser Ser Leu Ala Val Thr Thr Ile Asp
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Ile Arg Thr Leu Ile Asn Ile Thr Leu Ser Gln Asn Asn Leu Asn Gly
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Thr Ile Asp Ser Ala Pro Leu Ser Leu Cys Ser Lys Leu Gln Asn Leu
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Ile Leu Asn Gln Asn Asn Phe Ser Gly Lys Leu Pro Glu Phe Ser Pro
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Gly Glu Ile Pro Gln Ser Tyr Gly Arg Leu Thr Ala Leu Gln Val Leu
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Tyr Leu Thr Glu Leu Thr Arg Leu Asp Leu Ala Tyr Ile Ser Phe Asp
195 200 205

Pro Ser Pro Ile Pro Ser Thr Leu Gly Asn Leu Ser Asn Leu Thr Asp
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Leu Arg Leu Thr His Ser Asn Leu Val Gly Glu Ile Pro Asp Ser Ile
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Met Asn Leu Val Leu Leu Glu Asn Leu Asp Leu Ala Met Asn Ser Leu
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Thr Gly Glu Ile Pro Glu Ser Ile Gly Arg Leu Glu Ser Val Tyr Gln
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Gly Asn Leu Thr Glu Leu Arg Asn Phe Asp Val Ser Gln Asn Asn Leu
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Thr Gly Glu Leu Pro Glu Lys Ile Ala Ala Leu Gln Leu Ile Ser Phe
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Asp Val Ser Thr Asn Arg Phe Ser Gly Glu Leu Pro Pro Tyr Leu Cys
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Tyr Arg Arg Lys Leu Gln Lys Ile Ile Thr Phe Ser Asn Gln Leu Ser
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Ser Lys Arg Glu Thr Arg Tyr Ile Leu Pro Ile Ser Ile Leu Cys Ile
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Asn Ile Ile Gly Ser Gly Gly Ser Gly Leu Val Tyr Arg Val Lys Leu
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Ala Asp Phe Gly Leu Ala Lys Pro Leu Lys Arg Glu Asp Asn Asp Gly
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Val Ser Asp Val Ser Met Ser Cys Val Ala Gly Ser Tyr Gly Tyr Ile
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Ala Pro Glu Tyr Gly Tyr Thr Ser Lys Val Asn Glu Lys Ser Asp Val
850 855 860

Tyr Ser Phe Gly Val Val Leu Leu Glu Leu Ile Thr Gly Lys Arg Pro
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Glu Ala Ala Leu Cys Tyr Pro Ser Pro Ser Ala Glu Asp Gly Ala Met
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Asn Gln Asp Ser Leu Gly Asn Tyr Arg Asp Leu Ser Lys Leu Val Asp
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Pro Lys Met Lys Leu Ser Thr Arg Glu Tyr Glu Glu Ile Glu Lys Val
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